

OM protein - protein search, using sw model

Run on: May 24, 2004, 15:01:39 ; Search time 50.6667 Seconds  
(without alignments)  
3886.887 Million cell updates/sec

Title: US-09-806-194A-16  
Perfect score: 3651  
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3651	100.0	697	3	AAy88428	Aay88428 Human APP
2	3651	100.0	697	4	AAU07208	Aau07208 Human bet
3	3651	100.0	697	4	AAE10635	Aae10635 Human amy
4	3651	100.0	697	4	AAE06865	Aae06865 Human amy
5	3651	100.0	697	4	AAE02587	Aae02587 Human amy
6	3651	100.0	697	4	AAU06609	Aau06609 Human Amy
7	3651	100.0	697	5	ABB78596	Abb78596 Human APP
8	3646	99.9	697	3	AAy88430	Aay88430 Human APP
9	3646	99.9	697	4	AAU07210	Aau07210 Human bet

10	3646	99.9	697	4	AAE10637	Aae10637	Human	amy
11	3646	99.9	697	4	AAE06867	Aae06867	Human	amy
12	3646	99.9	697	4	AAE02589	Aae02589	Human	amy
13	3646	99.9	697	4	AAU06611	Aau06611	Human	Amy
14	3646	99.9	697	5	ABB78598	Abb78598	Human	APP
15	3646	99.9	740	7	ADB87314	Adb87314	Human	amy
16	3646	99.9	740	7	ADB87312	Adb87312	Human	amy
17	3643	99.8	697	3	AAAY88429	Aay88429	Human	APP
18	3643	99.8	697	4	AAU07209	Aau07209	Human	bet
19	3643	99.8	697	4	AAE10636	Aae10636	Human	amy
20	3643	99.8	697	4	AAE06866	Aae06866	Human	amy
21	3643	99.8	697	4	AAE02588	Aae02588	Human	amy
22	3643	99.8	697	4	AAU06610	Aau06610	Human	Amy
23	3643	99.8	697	5	ABB78597	Abb78597	Human	APP
24	3641	99.7	695	1	AAP81692	Aap81692	Sequence	
25	3641	99.7	695	2	AAR26338	Aar26338	APP695.	3
26	3641	99.7	695	2	AAAY20233	Aay20233	Human	bet
27	3641	99.7	695	2	AAAY07221	Aay07221	Amyloid	p
28	3641	99.7	695	3	AAAY88434	Aay88434	Human	APP
29	3641	99.7	695	3	AAAY44705	Aay44705	Human	bet
30	3641	99.7	695	4	AAE10632	Aae10632	Human	wil
31	3641	99.7	695	4	AAE06862	Aae06862	Human	wil
32	3641	99.7	695	4	AAE02584	Aae02584	Human	amy
33	3641	99.7	695	4	AAU06606	Aau06606	Human	Amy
34	3641	99.7	695	5	ABB78593	Abb78593	Human	APP
35	3641	99.7	695	5	AAG68315	Aag68315	Human	amy
36	3641	99.7	695	5	ABG32721	Abg32721	Human	amy
37	3641	99.7	695	6	ABP97918	Abp97918	Amino	aci
38	3641	99.7	695	6	ABB99604	Abb99604	Amino	aci
39	3641	99.7	695	7	ADB87311	Adb87311	Human	amy
40	3641	99.7	695	7	ADB33519	Adb33519	Human	APP
41	3641	99.7	695	7	ADC65997	Adc65997	Human	APP
42	3638	99.6	695	2	AAAY49690	Aay49690	Human	bet
43	3636	99.6	695	2	AAW19481	Aaw19481	APP695	mu
44	3636	99.6	695	2	AAW19484	Aaw19484	APP695	mu
45	3636	99.6	695	2	AAW19498	Aaw19498	APP695	mu

# ALIGNMENTS

## RESULT 1

AAAY88428

ID AAY88428 standard; protein; 697 AA.

XX

AC AAY88428;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human APP696-KK amino acid sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

KW Alzheimer's disease; beta secretase site; APP696-KK.

XX

OS Homo sapiens.

XX

PN WO200017369-A2.

XX PD 30-MAR-2000.  
XX  
PF 23-SEP-1999; 99WO-US020881.  
XX  
PR 24-SEP-1998; 98US-0101594P.  
XX  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
XX  
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;  
XX  
DR WPI; 2000-303209/26.  
DR N-PSDB; AAA15665.  
XX  
PT New enzyme designated human aspartase useful in research into Alzheimer's  
PT Disease is capable of cleaving amyloid protein precursor at the beta  
PT secretase site to produce amyloid beta peptide.  
XX  
PS Claim 132; Page 137-141; 183pp; English.  
XX  
CC This sequence represents a modified version of the human amyloid  
CC precursor protein (APP) amino acid sequence. The sequence is used in an  
CC example of the method of the invention, to show that modification of APP  
CC increases beta amyloid protein processing. The invention relates to a  
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of  
CC amyloid precursor protein (APP). The protease contains a sequence  
CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG  
CC separated by 100-300 amino acids. When mutated the APP gene causes an  
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell  
CC surface membrane and have a single C-terminal transmembrane domain.  
CC Proteolytic processing of APP produces the amyloid beta protein, which is  
CC possibly very important in Alzheimer's disease. The invention includes a  
CC nucleotide sequence encoding the protease, a vector containing the  
CC nucleotide sequence, and a cell line comprising the vector. Methods for  
CC screening for inhibitors of beta secretase activity are also given in the  
CC invention. The human aspartase protein and nucleotide sequences and the  
CC methods for identifying inhibitors of the protease, are useful in the  
CC treatment of and research in to Alzheimer's disease  
XX  
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 3; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.4e-253;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYQCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYQCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180

Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

# RESULT 2

AAU07208

ID AAU07208 standard; protein; 697 AA.

XX

AC AAU07208;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human beta-amyloid protein precursor, APP695-KK.

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease; APP695-KK.

XX

OS Homo sapiens.

XX

PN WO200149097-A2.

XX

PD 12-JUL-2001.

XX



PF 09-MAY-2001; 2001WO-IB000797.

XX

PR 09-MAY-2001; 2001WO-IB000797.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502548/55.

DR N-PSDB; AAS11708.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
PT activity.

XX

PS Example 6; Page 144-146; 185pp; English.

XX

CC The invention relates to a novel purified polypeptide comprising a  
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the  
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide  
CC and the fragment retain the beta-secretase activity of the mammalian Asp2  
CC protein. Also included is an isoform of amyloid protein precursor (APP)  
CC comprising the amino acid sequence of a APP or its fragment containing an  
CC APP cleavage site recognisable by a mammalian beta-secretase, and further  
CC comprising two lysine residues at the carboxyl terminus of the amino acid  
CC sequence of the mammalian APP or APP fragment. The polypeptides are used  
CC for assaying for modulators of beta-secretase activity; identifying  
CC agents that inhibit the APP processing activity of human Asp2 aspartyl  
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2  
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.  
CC Agents identified by the above methods are useful for treating  
CC Alzheimer's disease; and for identifying modulators of amyloid-beta  
CC (Abeta) peptide production, for use in designing therapeutics for the  
CC treatment or prevention of Alzheimer's disease. Probes and primers  
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp  
CC nucleic acids in in vitro assays and in Northern and Southern blots. The  
CC present sequence represents the amino acid sequence of human amyloid  
CC protein precursor, APP695-KK, used in the method of the invention

XX

SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;

Best Local Similarity 100.0%; Pred. No. 1.4e-253;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPG LALLLLA AWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSG TK 60
          |||
Db      1 MLPG LALLLLA AWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSG TK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
          |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
```

Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGHV	660
Db	601	RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGHV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

# RESULT 3

AAE10635

ID AAE10635 standard; protein; 697 AA.

XX

AC AAE10635;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human amyloid protein precursor 695-KK (APP695-KK) isoform.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP695-KK;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

XX

OS Homo sapiens.

OS Synthetic.  
 XX  
 PN GB2357767-A.  
 XX  
 PD 04-JUL-2001.  
 XX  
 PF 22-SEP-2000; 2000GB-00023315.  
 XX  
 PR 23-SEP-1999; 99US-00404133.  
 PR 23-SEP-1999; 99US-0155493P.  
 PR 23-SEP-1999; 99WO-US020881.  
 PR 13-OCT-1999; 99US-00416901.  
 PR 06-DEC-1999; 99US-0169232P.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Bienkowski MJ, Gurney M;  
 XX  
 DR WPI; 2001-444208/48.  
 DR N-PSDB; AAD17871.  
 XX  
 PT Polypeptide comprising fragments of human aspartyl protease with amyloid  
 PT precursor protein processing activity and alpha-secretase activity, for  
 PT identifying modulators useful in treating Alzheimer's disease.  
 XX  
 PS Example 6; Page 114-116; 187pp; English.  
 XX  
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1  
 CC proteins which lack transmembrane domain or amino terminal domain or  
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid  
 CC protein precursor (APP) processing activity. The proteins of the  
 CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which  
 CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase  
 CC activity, where modulators that increase hu-Asp1 alpha-secretase activity  
 CC are useful for treating Alzheimer's disease (AD) which causes progressive  
 CC dementia with consequent formation of amyloid plaques, neurofibrillary  
 CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful  
 CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein  
 CC with the substrate under acidic conditions and determining the level of  
 CC hu-Asp1 proteolytic activity. The present sequence is human amyloid  
 CC protein precursor 695-KK (APP695-KK) isoform which is obtained by the  
 CC addition of two Lys residues (KK motif) at the C-terminus of APP695  
 CC protein  
 XX  
 SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-253;  
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK 60  
 Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQIVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQIVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGHV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGHV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

#### RESULT 4

AAE06865

ID AAE06865 standard; protein; 697 AA.

XX

AC AAE06865;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human amyloid precursor protein 695-KK (APP695-KK) isoform.

XX

KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;

KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;

KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;

KW neuroprotective; antisense therapy; gene therapy; APP695-KK; mutant;

KW mutein.

XX  
 OS Homo sapiens.  
 XX  
 PN WO200150829-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000799.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000799.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-483072/52.  
 DR N-PSDB; AAD13027.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Example 6; Page 144-146; 185pp; English.  
 XX  
 CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid  
 CC precursor protein (APP) isoforms and their corresponding DNA molecules.  
 CC Human aspartyl proteases can act as beta-secretase proteases useful for  
 CC treating Alzheimer's disease. APP isoforms are useful for identifying  
 CC modulators of amyloid-beta peptide production, for use in designing  
 CC therapeutics for the treatment and prevention of Alzheimer's disease,  
 CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis  
 CC and neuronal loss. APP isoforms are also used in methods for identifying  
 CC inhibitors and modulators of human Asp2 activity. The invention relates  
 CC to a method for identifying agents that modulate the activity of human  
 CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used  
 CC as a means to screen in cellular assays for the inhibitors of beta- and  
 CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in  
 CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-  
 CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.  
 CC The present sequence is modified human amyloid precursor protein 695-KK  
 CC (APP695-KK) isoform. APP695-KK isoform is obtained by addition of two Lys  
 CC residues (KK motif) at the C-terminal end of APP695 isoform  
 XX  
 SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-253;  
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEEPVEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLVPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLVPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 5

AAE02587

ID AAE02587 standard; protein; 697 AA.

XX

AC AAE02587;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human amyloid precursor protein 695-KK (APP695-KK).

XX

KW Human; alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;

KW therapy; Alzheimer's disease; antialzheimer's.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200123533-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 22-SEP-2000; 2000WO-US026080.  
 XX  
 PR 23-SEP-1999; 99US-0155493P.  
 PR 23-SEP-1999; 99WO-US020881.  
 PR 13-OCT-1999; 99US-00416901.  
 PR 06-DEC-1999; 99US-0169232P.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Gurney M, Bienkowski MJ;  
 XX  
 DR WPI; 2001-290516/30.  
 DR N-PSDB; AAD06745.  
 XX  
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor  
 PT protein, useful for the treatment of Alzheimer's disease.  
 XX  
 PS Example 6; Page 143-145; 189pp; English.  
 XX  
 CC The present invention relates to enzymes for cleaving the alpha-  
 CC secretase site of the amyloid precursor protein (APP) and methods of  
 CC identifying those enzymes. The methods may be used to identify enzymes  
 CC that may be used to cleave the alpha-secretase cleavage site of the APP  
 CC protein. The enzymes may be used to treat or modulate the progress of  
 CC Alzheimer's disease. The present sequence is human APP695-KK. This  
 CC sequence contains two carboxy-terminal lysine residues  
 XX  
 SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-253;  
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240

Qy	241	EADDDDEDDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVLELLPVNGEFS	540
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVLELLPVNGEFS	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHG	660
Db	601	RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHG	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

# RESULT 6

AAU06609

ID AAU06609 standard; protein; 697 AA.

XX

AC AAU06609;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human Amyloid precursor protein mutant, APP695-KK.

XX

KW Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;  
 KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;  
 KW amyloid-beta; Abeta; APP695-KK; mutant; mutein.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 696..697

FT /note= "2 Extra Lys residues added compared to wild-type

FT APP695"

XX

PN WO200149098-A2.

XX



PD 12-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-502549/55.  
 DR N-PSDB; AAS11523.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Example 6; Page 144-146; 185pp; English.  
 XX  
 CC The invention relates to a purified polypeptide comprising a fragment of  
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2  
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and  
 CC the fragment retain the beta-secretase activity of the mammalian Asp2  
 CC protein. The invention also details polynucleotides for the Asp proteins  
 CC and vectors expressing them, and a polypeptide (isoform of amyloid  
 CC protein precursor (APP)) comprising the amino acid sequence of an APP or  
 CC its fragment containing an APP cleavage site recognizable by a mammalian  
 CC beta-secretase, and further comprising two lysine residues at the  
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP  
 CC fragment. Also included in the invention are methods of identifying  
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are  
 CC useful for treating Alzheimer's disease. APP is useful in methods for  
 CC identifying inhibitors or modulators of human Asp2 activity and amyloid-  
 CC beta (Abeta) peptide production. APP is also useful in designing  
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP  
 CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is  
 CC associated with increased levels of Abeta processing is useful in assays  
 CC relating the Alzheimer's research. The expression vector is useful for  
 CC recombinantly expressing APP. Nucleic acids that hybridise to Asp  
 CC oligonucleotides are useful as probes or primers. The probes are useful  
 CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and  
 CC Southern blots. The present sequence is the human APP695 mutant, APP695-  
 CC KK which has 2 extra Lys residues added at the C-terminus compared to the  
 CC wild-type APP695. The mutation alters the specificity of the APP gamma-  
 CC secretase activity and increases the rate of processing of the amyloid  
 CC Abeta peptide  
 XX  
 SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 4; Length 697;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-253;  
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRI SYGNDALMPSLTETKTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRI SYGNDALMPSLTETKTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 7

ABB78596

ID ABB78596 standard; protein; 697 AA.

XX

AC ABB78596;

XX

DT 16-JUL-2002 (first entry)

XX  
 DE Human APP695-KK protein sequence SEQ ID NO:16.  
 XX  
 KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;  
 KW amyloid precursor protein; APP.  
 XX  
 OS Homo sapiens.  
 XX  
 PN GB2367060-A.  
 XX  
 PD 27-MAR-2002.  
 XX  
 PF 29-OCT-2001; 2001GB-00025934.  
 XX  
 PR 23-SEP-1999; 99US-00404133.  
 PR 23-SEP-1999; 99US-0155493P.  
 PR 23-SEP-1999; 99WO-US020881.  
 PR 13-OCT-1999; 99US-00416901.  
 PR 06-DEC-1999; 99US-0169232P.  
 PR 22-SEP-2000; 2000GB-00023315.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Bienkowski MJ, Gurney M;  
 XX  
 DR WPI; 2002-397167/43.  
 DR N-PSDB; ABL52463.  
 XX  
 PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl  
 PT protease activity, e.g. for the diagnosis of Alzheimer's disease.  
 XX  
 PS Example 6; Page 114-116; 182pp; English.  
 XX  
 CC The present invention describes a human aspartyl protease 1 (hu-Asp1)  
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,  
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-  
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1  
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with  
 CC (I) under acidic conditions; and (b) determining the level of hu-Asp1  
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a  
 CC nucleotide sequence that hybridises under stringent conditions to the non  
 CC -coding strand complementary to a defined 1804 nucleotide sequence (see  
 CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1  
 CC proteolytic activity and lacks nucleotides encoding a transmembrane  
 CC domain); (3) a purified polynucleotide (III') comprising a sequence that  
 CC hybridises under stringent conditions to (III) (the nucleotide sequence  
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding  
 CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)  
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or  
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease  
 CC substrate (I) may be used as an enzyme substrate in assays to detect  
 CC aspartyl protease activity, (II) and therefore diagnose diseases  
 CC associated with aberrant hu-Asp1 expression and activity such as  
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while  
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present  
 CC sequence represents human amyloid precursor protein APP695-KK, which is  
 CC given in an example from the present invention

XX  
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 5; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.4e-253;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRINMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRINMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGEDGEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGEDGEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLFFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLFFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 8

AA88430

ID AAY88430 standard; protein; 697 AA.

XX

AC AAY88430;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human APP695-VF-KK amino acid sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

KW Alzheimer's disease; beta secretase site; APP695-VF-KK.

XX

OS Homo sapiens.

XX

PN WO200017369-A2.

XX

PD 30-MAR-2000.

XX

PF 23-SEP-1999; 99WO-US020881.

XX

PR 24-SEP-1998; 98US-0101594P.

XX

PA (PHAA ) PHARMACIA & UPJOHN CO.

XX

PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2000-303209/26.

DR N-PSDB; AAA15667.

XX

PT New enzyme designated human aspartase useful in research into Alzheimer's

PT Disease is capable of cleaving amyloid protein precursor at the beta

PT secretase site to produce amyloid beta peptide.

XX

PS Claim 133; Page 148-153; 183pp; English.

XX

CC This sequence represents a modified version of the human amyloid  
CC precursor protein (APP) amino acid sequence. The sequence is used in an  
CC example of the method of the invention, to show that modification of APP  
CC increases beta amyloid protein processing. The invention relates to a  
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of  
CC amyloid precursor protein (APP). The protease contains a sequence  
CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG  
CC separated by 100-300 amino acids. When mutated the APP gene causes an  
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell  
CC surface membrane and have a single C-terminal transmembrane domain.  
CC Proteolytic processing of APP produces the amyloid beta protein, which is  
CC possibly very important in Alzheimer's disease. The invention includes a  
CC nucleotide sequence encoding the protease, a vector containing the  
CC nucleotide sequence, and a cell line comprising the vector. Methods for  
CC screening for inhibitors of beta secretase activity are also given in the  
CC invention. The human aspartase protein and nucleotide sequences and the  
CC methods for identifying inhibitors of the protease, are useful in the  
CC treatment of and research in to Alzheimer's disease

XX

SQ Sequence 697 AA;

Query Match

99.9%; Score 3646; DB 3; Length 697;

Best Local Similarity 99.9%; Pred. No. 3.3e-253;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVEFVCCPLAEESDNVDSADAEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDEDGDEVEEEAEEPYPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 EADDDDEDEDGDEVEEEAEEPYPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 QEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy    481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy    601 RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660

Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
        ||||||||||||||||||||||||||||||||||||||||||||
Db    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
```

RESULT 9

AAU07210

ID AAU07210 standard; protein; 697 AA.

XX

AC AAU07210;

XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human beta-amyloid protein precursor, APP695-VF-KK.  
 XX  
 KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;  
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;  
 KW beta-secretase; Alzheimer's disease; APP695-VF-KK.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 642  
 FT /note= "Wild type Val substituted by Phe"  
 XX  
 PN WO200149097-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000797.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000797.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-502548/55.  
 DR N-PSDB; AAS11710.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Example 8; Page 150-152; 185pp; English.  
 XX  
 CC The invention relates to a novel purified polypeptide comprising a  
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the  
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide  
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2  
 CC protein. Also included is an isoform of amyloid protein precursor (APP)  
 CC comprising the amino acid sequence of a APP or its fragment containing an  
 CC APP cleavage site recognisable by a mammalian beta-secretase, and further  
 CC comprising two lysine residues at the carboxyl terminus of the amino acid  
 CC sequence of the mammalian APP or APP fragment. The polypeptides are used  
 CC for assaying for modulators of beta-secretase activity; identifying  
 CC agents that inhibit the APP processing activity of human Asp2 aspartyl  
 CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2  
 CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.  
 CC Agents identified by the above methods are useful for treating  
 CC Alzheimer's disease; and for identifying modulators of amyloid-beta  
 CC (Abeta) peptide production, for use in designing therapeutics for the

CC treatment or prevention of Alzheimer's disease. Probes and primers  
 CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp  
 CC nucleic acids in in vitro assays and in Northern and Southern blots. The  
 CC present sequence represents the amino acid sequence of human amyloid  
 CC protein precursor, APP695-VF-KK, used in the method of the invention  
 XX  
 SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 4; Length 697;  
 Best Local Similarity 99.9%; Pred. No. 3.3e-253;  
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEDDSVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEDDSVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNLMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNLMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLFFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660
Db	601	RHDSGYEVHHQKLFFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697



Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 10

AAE10637

ID AAE10637 standard; protein; 697 AA.

XX

AC AAE10637;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human amyloid protein precursor 695-VF-KK (APP695-VF-KK) isoform.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;

KW APP695-VF-KK; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 642

FT /note= "Wild-type Val substituted with Phe"

XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-00023315.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA ) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2001-444208/48.

DR N-PSDB; AAD17873.

XX

PT Polypeptide comprising fragments of human aspartyl protease with amyloid

PT precursor protein processing activity and alpha-secretase activity, for

PT identifying modulators useful in treating Alzheimer's disease.

XX

PS Example 8; Page 120-122; 187pp; English.

XX

CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified Aspl

CC proteins which lack transmembrane domain or amino terminal domain or

CC cytoplasmic domain and retains alpha-secretase activity and amyloid

CC protein precursor (APP) processing activity. The proteins of the

CC invention are useful for assaying hu-Aspl alpha-secretase activity, which

CC in turn is useful for identifying modulators of hu-Aspl alpha-secretase



```

      |||
Db      541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
      |||
Qy      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660
      |||
Db      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
      |||
Qy      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
      |||
Db      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

```

RESULT 11

AAE06867

ID AAE06867 standard; protein; 697 AA.

XX

AC AAE06867;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform.

XX

KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-VF-KK;

KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;

KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;

KW neuroprotective; antisense therapy; gene therapy; APP695-VF-KK; mutant;

KW mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 642

FT /note= "Wild type Val substituted with Phe"

XX

PN WO200150829-A2.

XX

PD 19-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000799.

XX

PR 09-MAY-2001; 2001WO-IB000799.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-483072/52.

DR N-PSDB; AAD13029.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2



Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

RESULT 12

AAE02589

ID AAE02589 standard; protein; 697 AA.

XX

AC AAE02589;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human amyloid precursor protein 695-VF-KK (APP695-VF-KK).

XX

KW Human; alpha-secretase; therapy; amyloid precursor protein 695-VF-KK;

KW APP695-VF-KK; Alzheimer's disease; antialzheimer's.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA ) PHARMACIA & UPJOHN CO.

XX

PI Gurney M, Bienkowski MJ;

XX

DR WPI; 2001-290516/30.

DR N-PSDB; AAD06747.

XX

PT Enzymes that cleave the alpha-secretase site of the amyloid precursor  
PT protein, useful for the treatment of Alzheimer's disease.

XX

PS Example 8; Page 149-151; 189pp; English.

XX

CC The present invention relates to enzymes for cleaving the alpha-  
CC secretase site of the amyloid precursor protein (APP) and methods of  
CC identifying those enzymes. The methods may be used to identify enzymes  
CC that may be used to cleave the alpha-secretase cleavage site of the APP  
CC protein. The enzymes may be used to treat or modulate the progress of  
CC Alzheimer's disease. The present sequence is human APP695-VF-KK. This  
CC sequence is characterised by a V to F alteration at position 642 and  
CC contains two carboxy-terminal lysine residues

XX

SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 4; Length 697;  
Best Local Similarity 99.9%; Pred. No. 3.3e-253;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEE	240
Qy	241	EADDDDEDGDEVEEEAEEPYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEEPYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFS	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFS	540

Qy 541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 |||  
 Db 541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 |||  
 Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660  
 |||  
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660  
 |||  
 Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK 697  
 |||  
 Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK 697  
 |||

RESULT 13

AAU06611

ID AAU06611 standard; protein; 697 AA.

XX

AC AAU06611;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human Amyloid precursor protein mutant, APP695-VF-KK.

XX

KW Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;  
 KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;  
 KW amyloid-beta; Abeta; APP695-VF-KK; London mutant; mutant; mutein.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 642

FT /note= "Wild-type Val substituted by Phe"

FT Misc-difference 696. .697

FT /note= "2 Extra Lys residues added compared to wild-type

FT APP695"

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000798.

XX

PR 09-MAY-2001; 2001WO-IB000798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502549/55.

DR N-PSDB; AAS11525.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl





Db	241	EADDDDEDDGDEVEEEAEFPYEEATERTTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQIVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQIVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 14

ABB78598

ID ABB78598 standard; protein; 697 AA.

XX

AC ABB78598;

XX

DT 16-JUL-2002 (first entry)

XX

DE Human APP695-VF-KK protein sequence SEQ ID NO:20.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic; amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX

PF 29-OCT-2001; 2001GB-00025934.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.  
PR 22-SEP-2000; 2000GB-00023315.

XX

PA (PHAA ) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2002-397167/43.

DR N-PSDB; ABL52465.

XX

PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl  
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.

XX

PS Example 8; Page 120-122; 182pp; English.

XX

CC The present invention describes a human aspartyl protease 1 (hu-Asp1)  
CC substrate (I) which comprises a peptide of no more than 50 amino acids,  
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-  
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1  
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with  
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1  
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a  
CC nucleotide sequence that hybridises under stringent conditions to the non  
CC -coding strand complementary to a defined 1804 nucleotide sequence (see  
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1  
CC proteolytic activity and lacks nucleotides encoding a transmembrane  
CC domain); (3) a purified polynucleotide (III') comprising a sequence that  
CC hybridises under stringent conditions to (III) (the nucleotide sequence  
CC encodes a polypeptide further lacking a pro-peptide domain corresponding  
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)  
CC comprising (III) or (III'); and (5) a host cell (V) transformed or  
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease  
CC substrate (I) may be used as an enzyme substrate in assays to detect  
CC aspartyl protease activity, (II) and therefore diagnose diseases  
CC associated with aberrant hu-Asp1 expression and activity such as  
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while  
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present  
CC sequence represents human amyloid precursor protein APP695-VF-KK, which  
CC is given in an example from the present invention

XX

SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 5; Length 697;

Best Local Similarity 99.9%; Pred. No. 3.3e-253;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
          |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
          |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR 180
          |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR 180
```

Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAENERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAENERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVA	480
Qy	481	EEIQDEVDELLOKEQNYSDVLNMISEPRISYGNDAIMPSTETKTVELLPVNGEFS	540
Db	481	EEIQDEVDELLOKEQNYSDVLNMISEPRISYGNDAIMPSTETKTVELLPVNGEFS	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

RESULT 15

ADB87314

ID ADB87314 standard; protein; 740 AA.

XX

AC ADB87314;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human amyloid A4 precursor (APP) Swedish mutant protein with tags.

XX

KW amyloid precursor protein; APP; amino acid tag; gamma-secretase;

KW alpha-secretase; beta-secretase; C-terminal cleavage product; gammaCTF;

KW presenilin 1; Alzheimer's disease; beta-amyloid; senile plaque;

KW secretase inhibitor; APP biosynthesis; APP activity; human;

KW amyloid A4 precursor; Swedish mutant; mutant; mutein.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 595  
 FT /note= "Wild-type Lys substituted by Asn"  
 FT Misc-difference 596  
 FT /note= "Wild-type Met substituted by Leu"  
 FT Cleavage-site 645. .646  
 FT /note= "Cleavage of the APP protein between these two  
 FT residues by gamma-secretase produces gammaCTF"  
 FT Region 718. .731  
 FT /label= V5\_epitope\_tag  
 FT Region 735. .740  
 FT /label= Polyhistidine\_tag  
 XX  
 PN WO2003064681-A2.  
 XX  
 PD 07-AUG-2003.  
 XX  
 PF 31-JAN-2003; 2003WO-GB000433.  
 XX  
 PR 31-JAN-2002; 2002GB-00002276.  
 XX  
 PA (EISA ) EISAI LONDON RES LAB LTD.  
 XX  
 PI Lucas FR, Taylor J;  
 XX  
 DR WPI; 2003-663492/62.  
 XX  
 PT New protein comprising an amyloid precursor protein and an amino acid  
 PT tag, useful for screening or identifying therapeutic compounds,  
 PT particularly secretase inhibitors, useful for the treatment of diseases  
 PT e.g. Alzheimer's disease.  
 XX  
 PS Claim 4; Page; 24pp; English.  
 XX  
 CC This invention relates to a novel protein which comprises an amyloid  
 CC precursor protein (APP) and an amino acid tag. The present invention also  
 CC relates to assays for measuring gamma-secretase activity and/or  
 CC simultaneously measuring alpha, beta or gamma-secretase activity which  
 CC involve utilising the stabilisation of the gamma-secretase C-terminal  
 CC cleavage product of APP (gamma C-terminal fragment of APP; gammaCTF).  
 CC GammaCTF is generated by the action of gamma-secretase/presenilin 1, an  
 CC important enzyme in Alzheimer's disease. GammaCTF is the sister product  
 CC of beta-amyloid which is produced by the same process and accumulates in  
 CC senile plaques in Alzheimer's disease. The protein or the methods of the  
 CC invention may be useful for screening a test compound for its ability to  
 CC modulate alpha, beta or gamma-secretase activity. In particular, the  
 CC protein or methods are useful for screening or testing secretase  
 CC inhibitors, and differentiating such inhibitors from agents that act  
 CC indirectly, for example interface with normal APP biosynthesis and  
 CC activity. The amino acid tag of the new protein is useful for the  
 CC stabilisation of gamma-secretase cleavage products of APP. Specifically,  
 CC the protein or methods may be useful for screening or identifying  
 CC therapeutic compounds or compositions for the treatment of diseases such  
 CC as Alzheimer's disease. The present sequence is that of the Swedish  
 CC mutant human amyloid A4 precursor (APP) of the invention, tagged with a  
 CC V5 epitope tag and a polyhistidine tag, which was expressed in KEK293  
 CC cells during the exemplification of the invention. Note: This sequence  
 CC does not appear in the specification but was created by the indexer from

CC information given.  
XX  
SQ Sequence 740 AA;

Query Match 99.9%; Score 3646; DB 7; Length 740;  
Best Local Similarity 100.0%; Pred. No. 3.6e-253;  
Matches 696; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEE	240
Qy	241	EADDDDEDGEDGEVEEEAEPPYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGEDGEVEEEAEPPYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660
Db	601	RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNK	696
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNK	696

Search completed: May 24, 2004, 15:11:16  
Job time : 52.6667 secs

OM protein - protein search, using sw model

Run on: May 24, 2004, 15:08:40 ; Search time 17 Seconds  
(without alignments)  
2116.665 Million cell updates/sec

Title: US-09-806-194A-16  
Perfect score: 3651  
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3651	100.0	697	4	US-09-548-372D-16	Sequence 16, Appl
2	3651	100.0	697	4	US-09-548-367D-16	Sequence 16, Appl
3	3651	100.0	697	4	US-09-551-853D-16	Sequence 16, Appl
4	3646	99.9	697	4	US-09-548-372D-20	Sequence 20, Appl
5	3646	99.9	697	4	US-09-548-367D-20	Sequence 20, Appl
6	3646	99.9	697	4	US-09-551-853D-20	Sequence 20, Appl
7	3643	99.8	697	4	US-09-548-372D-18	Sequence 18, Appl
8	3643	99.8	697	4	US-09-548-367D-18	Sequence 18, Appl
9	3643	99.8	697	4	US-09-551-853D-18	Sequence 18, Appl
10	3641	99.7	695	1	US-08-123-702-2	Sequence 2, Appli
11	3641	99.7	695	2	US-08-104-165-1	Sequence 1, Appli

12	3641	99.7	695	3	US-08-464-250-1	Sequence 1, Appli
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14	3641	99.7	695	4	US-09-458-481B-7	Sequence 7, Appli
15	3641	99.7	695	4	US-09-458-481B-8	Sequence 8, Appli
16	3641	99.7	695	4	US-09-548-372D-10	Sequence 10, Appl
17	3641	99.7	695	4	US-09-548-367D-10	Sequence 10, Appl
18	3641	99.7	695	4	US-09-551-853D-10	Sequence 10, Appl
19	3641	99.7	695	4	US-09-415-099-6	Sequence 6, Appli
20	3641	99.7	695	6	5218100-2	Patent No. 5218100
21	3636	99.6	695	4	US-09-548-372D-14	Sequence 14, Appl
22	3636	99.6	695	4	US-09-548-367D-14	Sequence 14, Appl
23	3636	99.6	695	4	US-09-551-853D-14	Sequence 14, Appl
24	3635	99.6	694	1	US-08-339-152A-18	Sequence 18, Appl
25	3635	99.6	694	2	US-08-007-999B-5	Sequence 5, Appli
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27	3633	99.5	695	4	US-09-548-372D-12	Sequence 12, Appl
28	3633	99.5	695	4	US-09-548-367D-12	Sequence 12, Appl
29	3633	99.5	695	4	US-09-551-853D-12	Sequence 12, Appl
30	3629	99.4	695	1	US-08-371-930-27	Sequence 27, Appl
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32	3617	99.1	695	1	US-08-339-152A-30	Sequence 30, Appl
33	3612	98.9	753	4	US-09-548-372D-61	Sequence 61, Appl
34	3612	98.9	753	4	US-09-548-367D-61	Sequence 61, Appl
35	3612	98.9	753	4	US-09-551-853D-61	Sequence 61, Appl
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37	3602	98.7	751	2	US-08-104-165-2	Sequence 2, Appli
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42	3602	98.7	751	4	US-08-832-867-5	Sequence 5, Appli
43	3602	98.7	751	4	US-09-548-372D-57	Sequence 57, Appl
44	3602	98.7	751	4	US-09-548-367D-57	Sequence 57, Appl
45	3602	98.7	751	4	US-09-551-853D-57	Sequence 57, Appl

#### ALIGNMENTS

RESULT 1  
 US-09-548-372D-16  
 ; Sequence 16, Application US/09548372D  
 ; Patent No. 6420534  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GURNEY ET AL.  
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
 AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: 29915/6280I  
 ; CURRENT APPLICATION NUMBER: US/09/548,372D  
 ; CURRENT FILING DATE: 2000-04-12  
 ; PRIOR APPLICATION NUMBER: US 60/155,493  
 ; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: US 09/404,133  
 ; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881  
 ; PRIOR FILING DATE: 1999-09-23



; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-548-372D-16

Query Match 100.0%; Score 3651; DB 4; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.4e-266;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
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Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV	300
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Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
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Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
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Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660

QY           661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK         697  
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 Db 541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVLMLKKKQYTSIHHGV 660  
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 Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNKK 697

RESULT 3

US-09-551-853D-16

; Sequence 16, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
 AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-551-853D-16

Query Match 100.0%; Score 3651; DB 4; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.4e-266;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

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Qy     121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db     121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy     181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db     181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

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RESULT 4  
US-09-548-372D-20  
; Sequence 20, Application US/09548372D

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; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-20

```

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Query Match          99.9%;  Score 3646;  DB 4;  Length 697;
Best Local Similarity 99.9%;  Pred. No. 3.4e-266;
Matches 696;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDGEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300
        |||
Db    241 EADDDDEDGEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
        |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
        |||
Db    361 QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

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Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480  
 |||  
 Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy 481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGN DALMP SLTETKT TVELL PVNGE FSL 540  
 |||  
 Db 481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGN DALMP SLTETKT TVELL PVNGE FSL 540

Qy 541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 |||  
 Db 541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660  
 |||  
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV 660

Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK 697  
 |||  
 Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQM QNKK 697

RESULT 5

US-09-548-367D-20  
 ; Sequence 20, Application US/09548367D  
 ; Patent No. 6440698  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GURNEY ET AL.  
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
 AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: 29915/6280H  
 ; CURRENT APPLICATION NUMBER: US/09/548,367D  
 ; CURRENT FILING DATE: 2000-04-12  
 ; PRIOR APPLICATION NUMBER: US 60/155,493  
 ; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: US 09/404,133  
 ; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881  
 ; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: US 60/101,594  
 ; PRIOR FILING DATE: 1998-09-24  
 ; NUMBER OF SEQ ID NOS: 73  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 20  
 ; LENGTH: 697  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-548-367D-20

Query Match 99.9%; Score 3646; DB 4; Length 697;  
 Best Local Similarity 99.9%; Pred. No. 3.4e-266;  
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGR LNMH MNVQNGKWDSDPSG TK 60  
 |||  
 Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGR LNMH MNVQNGKWDSDPSG TK 60

Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK	420
Db	361	QEKVESLEQEAAERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697

RESULT 6

US-09-551-853D-20

; Sequence 20, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-551-853D-20

Query Match 99.9%; Score 3646; DB 4; Length 697;  
Best Local Similarity 99.9%; Pred. No. 3.4e-266;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600



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Db      541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Qy      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660
Db      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
Qy      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
Db      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

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RESULT 7

US-09-548-372D-18

; Sequence 18, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-548-372D-18

Query Match 99.8%; Score 3643; DB 4; Length 697;

Best Local Similarity 99.7%; Pred. No. 5.7e-266;

Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHMNVQNGKWDSDPSGTK 60
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHMNVQNGKWDSDPSGTK 60
Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE 240

```

Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

RESULT 8

US-09-548-367D-18

; Sequence 18, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-548-367D-18

Query Match 99.8%; Score 3643; DB 4; Length 697;  
Best Local Similarity 99.7%; Pred. No. 5.7e-266;  
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
      |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVVEVAEEEEVAEVEEE 240
      |||
Db    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV 300
      |||
Db    241 EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
      |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAAENERQQIVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
      |||
Db    361 QEKVESLEQEAAENERQQIVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
      |||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
      |||
Db    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
      |||
Db    541 DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF 600

Qy    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKQYTSIHHGV 660
      |||
Db    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKQYTSIHHGV 660

Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
      |||
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Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 9

US-09-551-853D-18

; Sequence 18, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-551-853D-18

Query Match 99.8%; Score 3643; DB 4; Length 697;

Best Local Similarity 99.7%; Pred. No. 5.7e-266;

Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      |||
Db    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV 300
      |||
Db    241 EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
      |||
```

Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Qy	481	EEIQDEVDELLOKEQNYSDDVLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLOKEQNYSDDVLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVNLDAEF	600
Qy	601	RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK	697
Db	661	VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMQNKK	697

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: TSI121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-123-702-2

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Query Match          99.7%; Score 3641; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 8e-266;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVVEVAEEEEVAEVEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
        |||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
        |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
        |||
Db    361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
        |||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
        |||
Db    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

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Db          541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
QY          601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660
Db          601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660
QY          661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695
Db          661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695

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RESULT 11

US-08-104-165-1

; Sequence 1, Application US/08104165

; Patent No. 5877015

; GENERAL INFORMATION:

; APPLICANT: HARDY, John Anthony

; APPLICANT: GOATE, Alison Mary

; APPLICANT: MULLAN, Michael John

; APPLICANT: CHARTIER-HARLIN, Marie-Christine

; APPLICANT: OWEN, Michael John

; TITLE OF INVENTION: Test and Model for Alzheimer's Disease

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/104,165

; FILING DATE: 21-JAN-1992

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 9101307.8

; FILING DATE: 21-JAN-1991

; APPLICATION NUMBER: 9118445.7

; FILING DATE: 28-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebeschuetz, Joe

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 16163-000100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 695 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-104-165-1

Query Match 99.7%; Score 3641; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 8e-266;  
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695

RESULT 12



US-08-464-250-1  
; Sequence 1, Application US/08464250  
; Patent No. 6107542  
; GENERAL INFORMATION:  
; APPLICANT: HARDY, John Anthony  
; APPLICANT: GOATE, Alison Mary  
; APPLICANT: MULLAN, Michael John  
; APPLICANT: CHARTIER-HARLIN, Marie-Christine  
; APPLICANT: OWEN, Michael John  
; TITLE OF INVENTION: Test and Model for Alzheimer's Disease  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,250  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/104,165  
; FILING DATE: 21-JAN-1992  
; APPLICATION NUMBER: 9101307.8  
; FILING DATE: 21-JAN-1991  
; APPLICATION NUMBER: 9118445.7  
; FILING DATE: 28-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joe  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 16163-000100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 695 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-464-250-1

Query Match 99.7%; Score 3641; DB 3; Length 695;  
Best Local Similarity 100.0%; Pred. No. 8e-266;  
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60  
|||||  
Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695

RESULT 13

US-08-464-250-1

; Sequence 1, Application US/08464250

; Patent No. 6300540

; GENERAL INFORMATION:

; APPLICANT: HARDY, John Anthony

; GOATE, Alison Mary

; MULLAN, Michael John

; CHARTIER-HARLIN, Marie-Christine

; OWEN, Michael John

; TITLE OF INVENTION: Test and Model for Alzheimer's Disease

; NUMBER OF SEQUENCES: 44

```

;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Townsend and Townsend Kourie and Crew
;      STREET: 379 Lytton Avenue
;      CITY: Palo Alto
;      STATE: California
;      COUNTRY: US
;      ZIP: 94301
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy Disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/464,250
;      FILING DATE: 05-Jun-1995
;      CLASSIFICATION: 435
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/104,165
;      FILING DATE: 21-JAN-1992
;      APPLICATION NUMBER: 9101307.8
;      FILING DATE: 21-JAN-1991
;      APPLICATION NUMBER: 9118445.7
;      FILING DATE: 28-AUG-1991
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Liebeschuetz, Joe
;      REGISTRATION NUMBER: 37,505
;      REFERENCE/DOCKET NUMBER: 16163-000100
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 326-2400
;      TELEFAX: (415) 326-2422
;
;      INFORMATION FOR SEQ ID NO: 1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 695 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;
;      MOLECULE TYPE: protein
;
;      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-464-250-1

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Query Match          99.7%;  Score 3641;  DB 4;  Length 695;
Best Local Similarity 100.0%;  Pred. No. 8e-266;
Matches 695;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1  MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
|
Db      1  MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
|
Qy     61  TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
|
Db     61  TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
|
Qy    121  EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|
Db    121  EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|
Qy    181  GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
|

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Db      181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
Qy      241 EADDDDEDDGDEVEEEAEEPVEEATERTTSIATTTTTTTTTSVEEVVRVPTTAASTPDAV 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 EADDDDEDDGDEVEEEAEEPVEEATERTTSIATTTTTTTTTSVEEVVRVPTTAASTPDAV 300
Qy      301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
Qy      361 QEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 QEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
Qy      421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
Qy      481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
Qy      541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
Qy      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
Qy      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

```

RESULT 14

US-09-458-481B-7

; Sequence 7, Application US/09458481B

; Patent No. 6310048

; GENERAL INFORMATION:

; APPLICANT: KUMAR, Vijaya B.

; TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION

; FILE REFERENCE: 16153-9250

; CURRENT APPLICATION NUMBER: US/09/458,481B

; CURRENT FILING DATE: 1999-12-09

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 695

; TYPE: PRT

; ORGANISM: Monkey

US-09-458-481B-7

Query Match 99.7%; Score 3641; DB 4; Length 695;

Best Local Similarity 100.0%; Pred. No. 8e-266;

Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60  
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 Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy 181 GVEFVCCPLAEESDNVDSADAEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 GVEFVCCPLAEESDNVDSADAEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy 241 EADDDDEDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 EADDDDEDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy 361 QEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRRLALENYITALQAVPPRPRHVFNMLK 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 QEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRRLALENYITALQAVPPRPRHVFNMLK 420

Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVA 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVA 480

Qy 481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy 541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKKQYTSIHHGV 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKKQYTSIHHGV 660

Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

RESULT 15

US-09-458-481B-8

; Sequence 8, Application US/09458481B

; Patent No. 6310048

; GENERAL INFORMATION:

; APPLICANT: KUMAR, Vijaya B.

; TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION

; FILE REFERENCE: 16153-9250

; CURRENT APPLICATION NUMBER: US/09/458,481B  
; CURRENT FILING DATE: 1999-12-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 695  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-458-481B-8

Query Match 99.7%; Score 3641; DB 4; Length 695;  
Best Local Similarity 100.0%; Pred. No. 8e-266;  
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLOKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLOKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFVFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFVFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660

Qy           661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695  
              |||||  
Db           661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695

Search completed: May 24, 2004, 15:16:04  
Job time : 19 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2004, 15:06:00 ; Search time 14.3333 Seconds  
(without alignments)  
4677.593 Million cell updates/sec

Title: US-09-806-194A-16  
Perfect score: 3651  
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMKNKK 697

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3641	99.7	695	1	A49795	Alzheimer's diseas
2	3590.5	98.3	770	1	QRHUA4	Alzheimer's diseas
3	3544	97.1	695	2	S00550	Alzheimer's diseas
4	3519	96.4	695	2	A27485	Alzheimer's diseas
5	3103	85.0	747	2	JH0773	Alzheimer's diseas
6	2105	57.7	484	4	A32761	hypothetical Alzhe
7	1728	47.3	763	2	A49321	amyloid beta (A4)
8	1716	47.0	765	2	S42880	amyloid precursor-
9	1704	46.7	751	2	A49974	beta-amyloid precu
10	1185	32.5	653	2	A46362	amyloid precursor-
11	1143	31.3	511	2	JC1404	CDEI-box DNA-bindi
12	817.5	22.4	686	2	T15795	hypothetical prote
13	747	20.5	886	2	A32758	beta-amyloid-like



14	706	19.3	246	2	S38344	CDEI-binding prote
15	411	11.3	82	2	PQ0438	Alzheimer's diseas
16	296.5	8.1	191	2	A35981	sperm membrane pro
17	283	7.8	57	2	E60045	Alzheimer's diseas
18	283	7.8	57	2	F60045	Alzheimer's diseas
19	283	7.8	57	2	G60045	Alzheimer's diseas
20	283	7.8	57	2	D60045	Alzheimer's diseas
21	283	7.8	57	2	A60045	Alzheimer's diseas
22	283	7.8	57	2	B60045	Alzheimer's diseas
23	217	5.9	42	2	PN0512	beta-amyloid prote
24	192.5	5.3	1110	2	I51116	NF-180 - sea lampr
25	186	5.1	5170	2	T15348	hypothetical prote
26	185.5	5.1	407	1	EDBEQ3	immediate-early pr
27	185.5	5.1	993	2	S49461	synaptonemal compl
28	182	5.0	522	2	T32444	hypothetical prote
29	175.5	4.8	802	1	S48529	NAB3 protein - yea
30	175.5	4.8	1188	2	T46608	zinc finger protei
31	174.5	4.8	464	2	H90279	microtubule bindin
32	174.5	4.8	884	2	T20405	hypothetical prote
33	174	4.8	579	2	JH0820	160K golgi antigen
34	174	4.8	1087	2	T30330	gelsolin-related p
35	173.5	4.8	793	1	JH0628	caldesmon - human
36	172	4.7	771	1	A33430	h-caldesmon - chic
37	172	4.7	784	2	PN0009	neurofilament trip
38	172	4.7	1182	2	T30189	myelin transcripti
39	171	4.7	1271	2	A45555	glutamate rich pro
40	170	4.7	1948	2	S00485	gene 11-1 protein
41	169.5	4.6	298	1	TPHUTC	troponin T, cardia
42	169.5	4.6	721	2	S29795	hypothetical prote
43	169	4.6	885	2	G71608	ATP-dept. acyl-CoA
44	169	4.6	1187	2	T46637	transcription fact
45	168.5	4.6	675	2	T03744	myoD protein inhib

#### ALIGNMENTS

##### RESULT 1

A49795

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C;Species: *Macaca fascicularis* (crab-eating macaque)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C;Accession: A49795

R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.

A;Reference number: A49795; MUID:91273117; PMID:1905108

A;Accession: A49795

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-695 <POD>

A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing

Query Match 99.7%; Score 3641; DB 1; Length 695;  
Best Local Similarity 100.0%; Pred. No. 4.2e-184;  
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK 60
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Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVDPKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121 EFVSDALLVDPKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE 240
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Db    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300
      |||
Db    241 EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
      |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
      |||
Db    361 QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
      |||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy    481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
      |||
Db    481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
      |||
Db    541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
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Db    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
      |||
Db    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
```

RESULT 2

QRHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor; proteinase nexin II (PN-II)

N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000

C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644

R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.  
Nucleic Acids Res. 17, 517-522, 1989

A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.

A;Reference number: S02260; MUID:89128427; PMID:2783775

A;Accession: S02260

A;Molecule type: DNA

A;Residues: 1-288,'V',365-770 <LEM1>

A;Cross-references: EMBL:X13466

A;Note: alternative splice form APP(695)

R;Lemaire, H.G.  
submitted to the EMBL Data Library, November 1988

A;Reference number: S05194

A;Accession: S05194

A;Molecule type: DNA

A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>

A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360

A;Note: alternative splice form APP(695)

R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A;Title: Characterization of the 5'-end region and the first two exons of the beta-protein precursor gene.

A;Reference number: A32277; MUID:89165870; PMID:2538123

A;Accession: A32277

A;Molecule type: DNA

A;Residues: 1-75 <LAF>

A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074

R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.

A;Reference number: A33260; MUID:89392030; PMID:2675837

A;Accession: A33260

A;Molecule type: DNA

A;Residues: 656-737 <JOH>

A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865

R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein diagnostic assays.

A;Reference number: A35486; MUID:90321244; PMID:2196878  
 A;Accession: A35486  
 A;Molecule type: DNA  
 A;Residues: 672-710 <PRE1>  
 A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
 Gene 87, 257-263, 1990  
 A;Title: Genomic organization of the human amyloid beta-protein precursor gene.  
 A;Reference number: I39451; MUID:90236318; PMID:2110105  
 A;Accession: I39452  
 A;Status: nucleic acid sequence not shown; translation not shown; translated  
 from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-770 <YOS1>  
 A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616  
 A;Accession: I39451  
 A;Status: nucleic acid sequence not shown; translation not shown; translated  
 from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>  
 A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615  
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
 Gene 102, 291-292, 1991  
 A;Reference number: A59020; MUID:91340168; PMID:1908403  
 A;Contents: annotation; erratum  
 A;Note: revised physical map for reference I39451  
 R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.;  
 van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.  
 Science 248, 1124-1126, 1990  
 A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral  
 hemorrhage, Dutch type.  
 A;Reference number: I39453; MUID:90260663; PMID:2111584  
 A;Accession: I39453  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 656-737 <LEV>  
 A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620  
 A;Note: a mutation with 693-Gln is presented  
 R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A;Title: A mutation in the amyloid precursor protein associated with hereditary  
 Alzheimer's disease.  
 A;Reference number: I59562; MUID:92022553; PMID:1925564  
 A;Accession: I59562  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 689-716, 'F', 718-737 <MUR>  
 A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721  
 R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.;  
 Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.;  
 Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma,  
 V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.;  
 Schellenberg, G.D.  
 Am. J. Hum. Genet. 51, 998-1014, 1992  
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds  
 for the APP gene region.  
 A;Reference number: A44017; MUID:93035397; PMID:1415269

A;Accession: A44017  
 A;Molecule type: DNA  
 A;Residues: 687-692,'G',694-718 <KAM1>  
 A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378  
 A;Experimental source: familial Alzheimer disease family SB  
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)  
 A;Accession: B44017  
 A;Molecule type: DNA  
 A;Residues: 687-718 <KAM2>  
 A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380  
 A;Experimental source: familial Alzheimer disease family LIT  
 A;Note: sequence extracted from NCBI backbone (NCBIP:115376)  
 A;Note: this sequence has a silent mutation  
 R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.;  
 Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.  
 Nature 325, 733-736, 1987  
 A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a  
 cell-surface receptor.  
 A;Reference number: A03134; MUID:87144572; PMID:2881207  
 A;Accession: A03134  
 A;Molecule type: mRNA  
 A;Residues: 1-288,'V',365-770 <KAN>  
 A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526  
 A;Note: alternative splice form APP(695)  
 R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A;Title: Molecular cloning and characterization of a cDNA encoding the  
 cerebrovascular and the neuritic plaque amyloid peptides.  
 A;Reference number: A29030; MUID:87231971; PMID:3035574  
 A;Accession: A29030  
 A;Molecule type: mRNA  
 A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>  
 A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540  
 A;Note: the authors translated the codon GAG for residue 647 as Asp  
 R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.  
 Science 235, 877-880, 1987  
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain  
 amyloid of Alzheimer's disease.  
 A;Reference number: A47584; MUID:87120328; PMID:3810169  
 A;Accession: A47584  
 A;Molecule type: mRNA  
 A;Residues: 674-756,'S',758-770 <GOL>  
 A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707  
 A;Experimental source: brain  
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop,  
 P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L.  
 Science 235, 880-884, 1987  
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage  
 near the Alzheimer locus.  
 A;Reference number: A47585; MUID:87120329; PMID:2949367  
 A;Accession: A47585  
 A;Molecule type: mRNA  
 A;Residues: 674-703 <TAN1>  
 A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958  
 R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang,  
 J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.  
 EMBO J. 7, 949-957, 1988

A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.  
 A;Reference number: S02638; MUID:88296437; PMID:2900137  
 A;Accession: S02638  
 A;Molecule type: mRNA  
 A;Residues: 672-678 <DYR>  
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.  
 Nature 331, 528-530, 1988  
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.  
 A;Reference number: S00707; MUID:88122640; PMID:2893290  
 A;Accession: S00707  
 A;Molecule type: mRNA  
 A;Residues: 286-344,'I',365-366 <TAN2>  
 A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612  
 A;Experimental source: promyelocytic leukemia cell line HL60  
 A;Note: alternative splice form APP(751)  
 R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.  
 Nature 331, 525-527, 1988  
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.  
 A;Reference number: S00925; MUID:88122639; PMID:2893289  
 A;Accession: S00925  
 A;Molecule type: mRNA  
 A;Residues: 1-344,'I',365-770 <PO2>  
 A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721  
 A;Note: alternative splice form APP(751)  
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.  
 A;Reference number: A38949; MUID:88122641; PMID:2893291  
 A;Accession: A38949  
 A;Molecule type: mRNA  
 A;Residues: 287-367 <KIT>  
 A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611  
 A;Experimental source: glioblastoma cell line  
 A;Note: alternative splice form APP(770)  
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.  
 A;Reference number: A30320  
 A;Accession: A30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 284-288,'V',365-770 <VIT1>  
 A;Accession: B30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 122-288,'V',365-770 <VIT2>  
 A;Accession: C30320  
 A;Status: not compared with conceptual translation

A;Molecule type: mRNA  
A;Residues: 606-770 <VIT3>  
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.  
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.  
A;Reference number: A31087; MUID:88124954; PMID:2893379  
A;Accession: A31087  
A;Molecule type: mRNA  
A;Residues: 507-770 <ZAI>  
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573  
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 655 as Ser  
A;Note: the cited Genbank accession number, J03594, is not in release 101.0  
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 98.3%; Score 3590.5; DB 1; Length 770;  
Best Local Similarity 90.1%; Pred. No. 2.1e-181;  
Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
      |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDEDGDEVEEEAEEPYYEATERTTSIATTTTTTTTESVEEVVR----- 288
      |||
Db    241 EADDDDEDEDGDEVEEEAEEPYYEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPC 300

Qy    289 ----- 288
Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
      :|||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy    346 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 405
      |||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

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Qy	406	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	465
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	466	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	525
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Qy	526	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	585
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	586	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIVITL	645
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIVITL	720
Qy	646	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	695
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770

### RESULT 3

S00550

Alzheimer's disease amyloid beta protein precursor - rat

N;Alternate names: beta-A4 amyloid protein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999

C;Accession: S00550; A41245; A39820; S46251

R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.

EMBO J. 7, 1365-1370, 1988

A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.

A;Reference number: S00550; MUID:88312583; PMID:2900758

A;Accession: S00550

A;Molecule type: mRNA

A;Residues: 1-695 <SHI>

A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617

R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.

Science 241, 223-226, 1988

A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.

A;Reference number: A41245; MUID:88264430; PMID:2968652

A;Accession: A41245

A;Molecule type: protein

A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>

A;Note: evidence for heparan sulfate attachment

R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A;Title: The beta-A4 amyloid precursor protein binding to copper.

A;Reference number: S46251; MUID:94320627; PMID:7913895

A;Contents: annotation; copper binding sites

A;Note: rat peptides were isolated but not sequenced

R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.

J. Biol. Chem. 266, 8464-8469, 1991

A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain.



Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGR_LNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCG_K_LNMHMNVQNGKWESDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP CGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVG GADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDSIDSADAEEDSDVWVG GADTDYADGGEDKVVEVAEEEEVADVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAE EEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EAEDDEDVEDGDEVEEEAE EEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600

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Qy      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660
      ||||:|||||
Db      601 GHDSGFVVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV 660

Qy      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695
      |||||
Db      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695

```

## RESULT 4

A27485

AZ7485  
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N;Alternate names: proteinase nexin II

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text\_change 13-Aug-1999

C;Accession: A27485; S19727; I49485

R; Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.

A;Reference number: A27485; MUID:88106489; PMID:3322280

A:Accession: A27485

A;Molecule type: mRNA

A;Residues: 1-695 <YAM>

A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085

A;Experimental source: brain

R; de Strooper, B.; van Leuven, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.

A:Reference number: S19727; MUID:92096458; PMID:1756177

A:Accession: S19727

A;Molecule type: mRNA

A;Molecule type: RNA  
A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695  
<STR>

A;Cross-references: EMBL:X59379

R; Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
Gene 112, 189-195, 1992

A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.

A:Reference number: I49485; MUID:92209998; PMID:1555768

A;Accession: I49485

A:Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

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A;Residues: 1-19 <RES>
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A:Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329

C; Genetics:

A;Map position: 16C3

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type  
proteinase inhibitor homology

C; Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 96.4%; Score 3519; DB 2; Length 695;

Best Local Similarity 96.8%; Pred. No. 1.1e-177;

Matches 673; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MLPGILALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK 60



A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression.  
A;Reference number: JH0773; MUID:93129227; PMID:1282805  
A;Accession: JH0773  
A;Molecule type: mRNA  
A;Residues: 1-747 <OKA>  
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151  
A;Experimental source: larva  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology  
C;Keywords: alternative splicing; amyloid  
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

```

Qy      558 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFA 617
          |||||||||||||||||||||||||||||||||||||||:|:|:|:| |||||||||||
Db      610 TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDSEYRHDYAYEVHHQKLVFFA 669

Qy      618 EDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGHGVVEVDAAVTPEERHLSKM 677
          |:|||||||||||||||||||||||||||||||||:|:|:|:| |||||||||||
Db      670 EEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHHGVVEVDAAVTPEERHLTKM 729

Qy      678 QQNGYENPTYKFFEQQMN 695
          |||||||
Db      730 QQNGYENPTYKFFEQQMN 747

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# RESULT 6

A32761

hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1990 #sequence\_revision 10-Apr-1996 #text\_change 10-Apr-1996

C;Accession: A32761

R;de Sauvage, F.; Octave, J.N.

Science 245, 651-653, 1989

A;Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted protein.

A;Reference number: A32761; MUID:89346754; PMID:2569763

A;Accession: A32761

A;Molecule type: mRNA

A;Residues: 1-484 <DES>

A;Cross-references: GB:M28373

A;Note: the authors translated the codon ATG for residue 433 as Leu

C;Comment: This is the hypothetical translation of a sequence believed to contain cloning artifacts.

C;Keywords: cloning artifact

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Query Match          57.7%;  Score 2105;  DB 4;  Length 484;
Best Local Similarity 87.7%;  Pred. No. 1.5e-103;
Matches 407;  Conservative 1;  Mismatches 0;  Indels 56;  Gaps 1;

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Qy      80 LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKFLHQE 139
          |||||||||||||||||||||||||||||||||||||||
Db      1  LQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKFLHQE 60

Qy     140 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 199
          |||||||||||||||||||||||||||||||||||
Db      61 RMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSA 120

Qy     200 DAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEEEEADDDDEDGDEVEEEEAE 259
          |||||||||||||||||||||||||||||||||||
Db     121 DAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEEEEADDDDEDGDEVEEEEAE 180

Qy     260 EPYEEATERTTSIATTTTTTTESVEEVVR----- 288
          |||||||||||||||||||
Db     181 EPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWFYFDVTEGKCAPF 240

Qy     289 -----VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 323
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     241 FYGGCGGNRRNFDTEEYCMVCGSAIPTTAASTPDAVDKYLETPGDENEHAHFQKAKERL 300

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Qy	324	EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM	383
Db	301	EAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHM	360
Qy	384	ARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV	443
Db	361	ARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMV	420
Qy	444	DPKKAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV	487
Db	421	DPKKAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEV	464

# RESULT 7

A49321

amyloid beta (A4) homolog 2 precursor - human

N;Alternate names: CDEI-binding protein

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 13-Aug-1999

C;Accession: A49321; S34644; S40519

R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster, D.C.

Biochemistry 32, 4481-4486, 1993

A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: evidence for a multigene family.

A;Reference number: A49321; MUID:93250009; PMID:8485127

A;Accession: A49321

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <SPR>

A;Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169

A;Experimental source: placenta

A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)

A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney

R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.

submitted to the EMBL Data Library, April 1993

A;Description: The human homologue of the murine CDEI binding protein is an amyloid precursor like protein.

A;Reference number: S34644

A;Accession: S34644

A;Molecule type: mRNA

A;Residues: 1-763 <VON>

A;Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764

R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.;

Hyman, B.T.; Neve, R.L.; Tanzi, R.E.

Nature Genet. 5, 95-99, 1993

A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's associated amyloid beta protein precursor.

A;Reference number: S40519; MUID:94035131; PMID:8220435

A;Accession: S40519

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <WAS>

A;Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392

C;Genetics:

A;Gene: GDB:APLP2; APPL2

A;Cross-references: GDB:139159; OMIM:104776

A;Map position: 11q23-11q25

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type  
proteinase inhibitor homology

C;Keywords: alternative splicing; transmembrane protein

F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.3%; Score 1728; DB 2; Length 763;

Best Local Similarity 47.1%; Pred. No. 1.7e-83;

Matches 372; Conservative 112; Mismatches 165; Indels 140; Gaps 20;

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Qy      5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
      | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db     15 LLLLLLVGLTAPALALAGYIEALANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74

Qy     57 SGTCTCIDTKEGILQYQCQEVYPQLITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
      : | | | | | : | | | : | | | | | | | | | | | | | | | | | | | | | |
Db     75 TGTKSCFETKEEVLQYQCQEMPQLITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK 132

Qy    117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    133 CLVGEFVSDVLLVPEKQCFHFKERMEVCENHQHWHVTVKEACLTQGMTLYSYGMLLPCGV 192

Qy    177 DKFRGVFEVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAE 236
      | : | | | : | | | | : : | | | : : | | | | : | | | |
Db    193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-----EEEEDEEEDYDVYKSEFPTEAD 245

Qy    237 VEE--EEA--DDDEDDDEDGDEVEEEAAEPPY-----EEATERTTSIATTTTTTTTES 282
      : | : | | : | | | | | : : | | | | | | | | | | | | | | |
Db    246 LEDFTEAAVDEDEDEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy    283 VEEV-----VRVP 290
      | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db    306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCKAMIP 365

Qy    291 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPK 350
      | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | |
Db    366 PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNMRMDRVKKEWEEAELQAKNLPK 424

Qy    351 ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPP 410
      | : : : : | | | | | : | | | | | | | | | | | | | | | | | | | |
Db    425 AERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRMALENYLAALQSDPP 484

Qy    411 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIYERMNQL 470
      | | : | : | | | | | | | | | | | | | | | | | | | | | | |
Db    485 RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQL 544

Qy    471 SLLYNVPAVAEEIQDEVDLQKEQNYSDVLANMISEPRISYGNLMPSLTETKTTVE 530
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    545 SLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTASISETPVDVR 587

Qy    531 LLPVNGEFSDDLQPDWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN----- 585
      | : | | | : : | | | | | | | | | | | | | | | | | | | |
Db    588 ---VSSEES-EEIPPFHPF--HPFPALPENE---DTQPELYHPM--KKGSGVGEQDGG 635

Qy    586 IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----NKG 625
      | | | | | : | | | | | : | | | | | : : : | | | | | | | | |
```

Qy	5	LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRILNMHMNVQNGKWDSDP	56
		:         :     :        :    :    :	
Db	15	LLVLLLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAMFCGKILNMHVNIQTGKWEPPD	74
Qy	57	SGTKTCIDTKEGILQYQCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR	116
		:   :  :   :    :    :    :    :    :    :    :    :    :    :    :	
Db	75	TGTKSCLGTKEEVLQYQCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK	132
Qy	117	CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI	176
		:  :      :             :  :  :      :    :    :	





A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid precursor protein (APP).  
A;Reference number: A49974; MUID:94132029; PMID:8300594  
A;Accession: A49974  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-751 <SLU>  
A;Cross-references: GB:U15571; NID:g558467; PIDN:AAA50603.1; PID:g558468  
A;Note: sequence extracted from NCBI backbone (NCBIP:144636)  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology  
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.7%; Score 1704; DB 2; Length 751;  
Best Local Similarity 45.9%; Pred. No. 3.1e-82;  
Matches 363; Conservative 113; Mismatches 159; Indels 156; Gaps 20;

```

Qy      5  LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWSDP 56
      | :|||  || | :          |||  :|||||||:||||:|:| |||: ||
Db      15  LLVLLLLGLTAPAAALAGYIEALANAGTGFVAEPAQIAMFCGKLNMHVNIQTGWEPDP 74

Qy      57  SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
      :|||:|: ||| :|||||:|||||||:||||| | :||:| ::|||: | |||:
Db      75  TGTKSCLGTKEEVLYQCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy     117  CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
      ||||| |||| | :| ||||:||| | |||: || | : |||||:
Db     133  CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSGMLLPCGV 192

Qy     177  DKFRGVEFVCCPLAE--ESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAE---E 231
      |:| | |:||| : :||: | : ||:  | | || : : :| |
Db     193  DQFHGTEYVCCPQTKTVSDSDTMSKEEEEEEE-----DEEDEEDYDLKSEFPTE 243

Qy     232  EEVAEEEEEEAD-DEDEDEDGDEVEEE-----AEPYEEATERTTSIATTT 276
      :: : | || :|||:|:| || :  | | | :| | |
Db     244  ADLEDFTEAAADEEEEEDEEGEEVVEDRDYYYDPFKGDYNEENPTEPSSEGTIS----- 298

Qy     277  TTTTESVEEV----- 286
      | | :|
Db     299  --DKEIVHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESDYC 356

Qy     287  -----VRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAA 341
      :| | | | | | | | | | :||| | ||||:| | :| | :| | |
Db     357  MAVCKAMIPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEAA 415

Qy     342  ERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENY 401
      | ||||| :: :||| | :|||:|:| |||||:|||||:|||||
Db     416  ELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRLALENY 475

Qy     402  ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
      : |||: ||| : | :||| | | ||:|:| | |||:||||:||||| |
Db     476  LAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHV 535

Qy     462  IYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPS 521
      | | ||||| | | | :|||:|:||||:| :| | |
Db     536  IEERNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTSS 578

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Qy      522 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGS 581
          ::|  | :  | :  | | |  | : :|||  | : : |
Db      579 ISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE-----GSGMAEQDG- 621

Qy      582 GLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----N 623
          ||  : : | | : |||  |  :|  ::::| || ||  :
Db      622 GLIGAEKVINSKNKMNDENMVIDETLDV--KEMIFNAERVGGLEEEEPESVGPLREDFSL 679

Qy      624 KGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYE 683
          |::||:|  | |||||:||||:|:| | | :|||  :|||||:||| :|||
Db      680 SNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHYGE 739

Qy      684 NPTYKFFEQQM 694
          |||||: ||||
Db      740 NPTYKYLEQQM 750

```

# RESULT 10

A46362

amyloid precursor-like protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Nov-1999

C;Accession: A46362

R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.  
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992

A;Title: Identification of a mouse brain cDNA that encodes a protein related to  
the Alzheimer disease-associated amyloid beta protein precursor.

A;Reference number: A46362; MUID:93066322; PMID:1279693

A;Accession: A46362

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-653 <WAS>

A;Experimental source: brain

A;Note: sequence inconsistent with the nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684)

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type  
proteinase inhibitor homology

C;Keywords: transmembrane protein

Query Match 32.5%; Score 1185; DB 2; Length 653;

Best Local Similarity 38.6%; Pred. No. 5e-55;

Matches 270; Conservative 121; Mismatches 231; Indels 78; Gaps 17;

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Qy      1  MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRINMHMNVQNGKWDSDPSGT 59
          :|| |:|||| | | | | :  |  |:|  ||| :| ::| |:|: ||  :
Db      22  LLP-LSLLLLRAQLAVGNLAVGSPSAEAPGSAQVAGLCGRITLHRDLRTGRWEPDPQRS 80

Qy      60  KTCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
          : | :  : :|:|:|:| | | :| | : :| |  |  ||| |:|: ||
Db      81  RRCLLDPQRVLEYCRQMPYELHIARVEQAAQAI PMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy      119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
          |||||:|||||: |:||||||| ||:  | |:| || :  ||  ||||| |:
Db      141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQAEACSSQGLILHSGMMLPCGSDR 200

Qy      179 FRGVEFVCCPLAEESDNVDSADAEEDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
          |||||:||||  : |  | :  : | ||  |:| ||  |||

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```

Db      201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR-----AEGGED-----EEEVESF 248
QY      238 EEEEADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVRVPTTAASTP 297
      : | : :| ||| || : | : : | | ||
Db      249 PQPVDDYFVEPPQAEEEEEEEERAPPPSSHTPVMVSRVTPTPR-----PT----- 294
QY      298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI 357
      | || | ||: || | :|| || : ::::| || | : | :||| ||:| :
Db      295 DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN 354
QY      358 QHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFN 417
      :||| ::||: : |||:|||| || |::||| || | : || | ||: |
Db      355 EHFQSILQTLQEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414
QY      418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
      |::|:||||:|:|:|:| |||:| | :| | |||:| | ||||| || |
Db      415 ALRRYLRAEQKEQRHTLRHYQHVAVDPEKAQQMRQVQTHLQVIEERMNQSIGLLDQNP 474
QY      478 AVAEIQDEVDPELLQKEQNYSDVLANMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
      :|:|: : || | || : : || :| | :| |
Db      475 HLAQELRPQIQELL-----LAEHLGPSEL----DASVPGSSSEDK----- 510
QY      537 EFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
      ||| |:::| | :| | : | | : : :
Db      511 ----GSLQP-----PESKDDPPVTLP---KGSTDQESSSSGREKLTPLEQYEQ 551
QY      597 DAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVM-LKKKQ 652
      |: | |: | :: |: ||: | ::||:|:| |||
Db      552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGGSLLVLSLLLLRKKKP 611
QY      653 YTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
      | : | ||||| :| ||: | ::::| |||||:| | :
Db      612 YGTISHGVVEVDPMLTLEEQQQLRELQRHGYENPTYRFLEE 651

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# RESULT 11

JC1404

CDEI-box DNA-binding protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Feb-1997

C;Accession: JC1404

R;Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.

Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992

A;Title: A murine sequence-specific DNA binding protein shows extensive local similarities to the amyloid precursor protein.

A;Reference number: JC1404; MUID:93129193; PMID:1482349

A;Accession: JC1404

A;Molecule type: mRNA

A;Residues: 1-511 <VID>

C;Comment: This protein plays an important role in the early development of the mouse.

C;Keywords: DNA binding; transmembrane protein

Query Match 31.3%; Score 1143; DB 2; Length 511;

Best Local Similarity 45.8%; Pred. No. 6e-53;

Matches 253; Conservative 92; Mismatches 128; Indels 80; Gaps 16;

Qy	174	CGIDKFRGVEFVCCPLAE--ESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAE-	230
Db	6	CGVDQFHGTEYVCCPQTKTVDS DSTMSKEEEEEEE-----DEEDEEEDYDLDKSEF	56
Qy	231	--EEEEVAEVEEEEAD-DEDEDDEGDEVEEEEAE-----EPYEEATERTTTSIATTTTTT	279
Db	57	PTEADLEDFTEAAADEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTIS	114
Qy	280	TESVEEVVRVPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWE	339
Db	115	DKEIVHDVKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWE	173
Qy	340	EAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALE	399
Db	174	EAEIQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRIALE	233
Qy	400	NYITALQAVPPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHL	459
Db	234	NYLAALQSDPPRPHRIQLALRRYVRAENKDRDLHTIRHYQHVLAVDPEKAAQMKSQVMTHL	293
Qy	460	RVIYERMNQSLSLLYNVPAAVEEIQDEVDPELLQKEQNYSDVLANMISEPRISYGNDAIM	519
Db	294	HVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFT	336
Qy	520	PSLTETKTTVELLPVNGEFLDDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRP	579
Db	337	SSISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE-----GSGMAEQD	380
Qy	580	GSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----	622
Db	381	G-GLIGAEKVINSKNKM DENMVIDETLDV--KEMIFNAERVGGLEEEPE SVGPLREDFS	437
Qy	623	-NKGAIIGLMVGGVVIATVIVITLVM LKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNG	681
Db	438	LSSNALIGLLVIAVAIATVIVISLVM LKRRQYGTISHGIVEVDPM LTPPEERHLNKM QNHG	497
Qy	682	YENPTYKFFEQMQ	694
Db	498	YENPTYKYLEQMQ	510

A;Experimental source: strain Bristol N2; clone C42D8  
 R;Daigle, I.; Li, C.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993  
 A;Title: apl-1, a *Caenorhabditis elegans* gene encoding a protein related to the human beta-amyloid protein precursor.  
 A;Reference number: A49414; MUID:94089766; PMID:8265668  
 A;Accession: A49414  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 7-686 <DAI>  
 A;Cross-references: GB:U00240; NID:g416296; PIDN:AAC46470.1; PID:g416297  
 C;Genetics:  
 A;Gene: CESP:C42D8.8  
 A;Map position: X  
 A;Introns: 22/3; 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3; 580/3  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

Query Match 22.4%; Score 817.5; DB 2; Length 686;  
 Best Local Similarity 29.1%; Pred. No. 1.1e-35;  
 Matches 222; Conservative 110; Mismatches 275; Indels 155; Gaps 22;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
		::    : :             :        :   :     :	
Db	6	LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA	63
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
		: ::    :   :    :  :: :             :	
Db	64	TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG	122
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN-----LHDYGMLLPC	174
		::       ::      :      :     : : :	
Db	123	EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC	182
Qy	175	GIDKFRGVFEVCCPLAESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEV	234
		:             :   :   ::	
Db	183	ALDMFTGVFEVCCP-----NDQTNKTDVQKTK-----	209
Qy	235	AEVEEEEADDDDEDEDGDEVEEEAEOPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAA	294
		:::         :   ::	
Db	210	---EDEDDEDDDDAYEDDYSEESDEKDEE-----	236
Qy	295	STPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA-----ERQAKNLP	349
		:     :       ::  ::   :::  ::    :   ::	
Db	237	-EPSSQDPYFKIANWTNEHDDFKKAEMRMDEKHKVVDKVMKEWGDLETRYNEQKAKD-P	294
Qy	350	KADKKAVIQ---HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL-	405
		:      ::     :   :::     :    :::     :	
Db	295	KGAEKFKSQMNARFQKTVSSLEEEHKMRMKEIEAVHEERVQAMLNEKKRDATHDYRQALA	354
Qy	406	-QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE	464
		:: ::       :   :    ::    :   :	
Db	355	THVNKPNKHSVLQSLKAYIRAEKDRMHTLNRYRHLLKADSKEAAAYKPTVIHRLRYIDL	414
Qy	465	RMNQSLSLLYNVP-----AVA--EEIQDEVDELLQKEQNYSDVLNLMISEPRISY	513
		::  :::  :      : :      :     :   :	

```

Db      415 RINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE----DSELTPIIHDDDEFSK 470
Qy      514 GN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANT---ENEVEP 564
      |  | : |   :   : : ||   | : :   : :   |   |   : : | :
Db      471 NAKLDVKAPT TTA KPVKETDN AKVLPTEASDSEEEADEYYEDEDDEQVKKTPDMKKKKVKV 530
Qy      565 VDARP-----AADRGLTTRPGSGLTNIKTEE-----ISEVKMDA 598
      || : |           |           | | : : : |   | | : : |
Db      531 VDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDESSSSSTSSSEDEDEDKNIKELRVDI 590
Qy      599 E-----FRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLK 649
      |           : |||   || :   |   |           : :   : | | |   :
Db      591 EPIIDEPASFYRHD-----KLIQSPEVER SASSVFQPYVLASAMFITAICIIAFAIT 642
Qy      650 KKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691
      :   | : |||   || ||| : : || || || || || || :
Db      643 NARRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTY SFFD 683

```

# RESULT 13

A32758

beta-amyloid-like protein precursor - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 08-Dec-1989 #sequence\_revision 08-Dec-1989 #text\_change 24-Sep-1998

C;Accession: A32758

R;Rosen, D.R.; Martin-Morris, L.; Luo, L.; White, K.

Proc. Natl. Acad. Sci. U.S.A. 86, 2478-2482, 1989

A;Title: A *Drosophila* gene encoding a protein resembling the human beta-amyloid protein precursor.

A;Reference number: A32758; MUID:89184650; PMID:2494667

A;Accession: A32758

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-886 <ROS>

A;Cross-references: GB:J04516; NID:g158371; PID:g158372

C;Genetics:

A;Gene: FlyBase:Appl

A;Cross-references: FlyBase:FBgn0000108

C;Keywords: transmembrane protein

Query Match 20.5%; Score 747; DB 2; Length 886;

Best Local Similarity 25.5%; Pred. No. 7.8e-32;

Matches 233; Conservative 127; Mismatches 288; Indels 264; Gaps 29;

```

Qy      7 LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHMNV-QNGKWDS D PSG 58
      ||| : |   | :   | | : |   || ||| : |   | : :   : : | : | |
Db      9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWVTDL SK 63
Qy     59 T---KTCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV 112
      || : |   : | || : : ||   ||| : || : :   |   || : : |   : ||   : :
Db     64 KTTGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAACKCKGSHRWI 123
Qy    113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGM L L 172
      | : ||| | | | || ||| : | | |   |   : | :   | | :   : : |||
Db    124 KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRTFAM L L 182
Qy    173 PCGIDKFRGVEFVCCP-----LAEESDNVD---SA 199

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```

      |||| | |||||
Db      183 PCGISVFSGVFEVCCPKHFKTDEIHVKKTDLPVMPAAQINSANDELMNDEDDSDNSNYSK 242
Qy      200 DAEEDDSDVWVGADTDYADGSEDKVVEVAEEEEV-----AEV 237
      || ||| | | | : : | : |
Db      243 DANEDDL-----DEDDLMGDDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINA EY 296
Qy      238 EE-EEADDEDEDGDEVEEEAE EPY-----EEATERT 269
      : || | : | : | | | : | : | : :
Db      297 DSGEEDNYEEDGAGSESEAEVEASWDQSGGAKVVSLSKSDSSSPSSAPVAPAPEKAPVKS 356
Qy      270 TSIATTTTTTTSVEEV-----RVPTTAASTPDAVDKYLETPGDENEHAHFQK 318
      | : : | : : | | : || | | | | : :
Db      357 ESVTSTPQLSASAAAFVAANSNGNSGTGAGAPPSTAQPTS---DPYFTHFDPHYEHQSYKV 413
Qy      319 AKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKA-----VIQHFQEKVESLEQEA 371
      : : ||| ||| : : | : | : : : || | : || | : |
Db      414 SQKRLEESHREKVTRVMKDWSDLEEKYQDMRLADPKAAQSFQRMRTARFQTSVQALEEEG 473
Qy      372 ANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQ 431
      | : || | || | : | : | : | || || || | : | : || |||
Db      474 NAEKHQLAAMHQQRVLAHINQRKREAMTCYTQALTEQPPNAHHVEKCLQKLLRALHKDRA 533
Qy      432 HTLKHFEB-VRMVD-----KKAQIRSQVMTHLRVIYERMNQSLSLLYNPVAEAEI----- 483
      | | | : | : | : || | : : | | : ||| : : | | : : |
Db      534 HALAHYRHLNNSGGPGGLEAAASERPTLERLIDIDRAVNQSMTMLKRYPELSAKIAQLM 593
Qy      484 -----QDEV----- 487
      : | : :
Db      594 NDYILALRSKDDIPGSSLGMSEAEAGILDKYRVEIERKVAEKERLRLAEKQRKEQRAAE 653
Qy      488 -----DELLQKEQNYSDDVLNMISE-----PRISYGNDAIM 519
      : | | : | || : : : | | | :
Db      654 REKLREEKLRLAEAKVDDMLKSQVAEQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAAAL 713
Qy      520 -----PSLTETKTTVELLPVNGEFLSDDLQPWHSFGADSVANTENEVEPVDARPAADRG 574
      | : | || : | | | : : | : | | | |
Db      714 VTAANPNLETTKS-----EKDLSDE-----YGEATVSTTKVQTVLPTVDDDAVQRA 760
Qy      575 LTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---GA 626
      : : : : : : : : | : : | | : |
Db      761 VEDVAAA-----VAHQEAEPQVQHFMTHDLGHRSSFSLLRREFAQHAAHAAKEGRNV 811
Qy      627 IIGLMVGGVVIATVIVITLVMLKKKQYTSIH-HGVVEVDAAVTP-----EERHLSKMQQ 679
      | | : : : : : | | | : ||| || || : : ||
Db      812 YFTLSFAGIALMAAFVGVAVAKWRTSRSPHAQGFIQVNDQNTTHHPVREEKIVPNMQI 871
Qy      680 NGYENPTYKFFE 691
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Db      872 NGYENPTYKYFE 883

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RESULT 14

S38344

CDEI-binding protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 03-May-1996



C;Accession: S38344  
R;Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.  
Biochim. Biophys. Acta 1216, 154-156, 1993  
A;Title: The complete cDNA coding sequence for the mouse CDEI binding protein.  
A;Reference number: S38344; MUID:94032480; PMID:8218408  
A;Accession: S38344  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-246 <HAN>  
A;Cross-references: EMBL:Z22592  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type  
proteinase inhibitor homology

Query Match 19.3%; Score 706; DB 2; Length 246;  
Best Local Similarity 51.5%; Pred. No. 2.2e-30;  
Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;

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Qy      5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWSDP 56
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Db      15 LLVLLLLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPPD 74

Qy      57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
      :|||:|: ||| :|||||:|||||||:||||| | :||:| ::|||: | |||::
Db      75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy     117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
      ||||| |||| | :| ||||:||| | |||: || | : | : ||||| |||
Db     133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSGMLLPCGV 192

Qy     177 DKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVEVEAEVEEVAE 236
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Db     193 DQFHGTEYVCCP---QTKTVDS-----DSTMSKEEEEE--- 222

Qy     237 VEEEEADDDDED-DEDGDEVEEEAE 259
      ||:| |:|| | | | ||:
Db     223 -EEDEEDEEEDYDLKSEFPTEAD 245

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# RESULT 15

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995

C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor protein gene.

A;Reference number: PQ0438; MUID:93075180; PMID:1445331

A;Accession: PQ0438

A;Molecule type: DNA

A;Residues: 1-82 <DAV>

A;Cross-references: GB:M83558; GB:M83657

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991



OM protein - protein search, using sw model

Run on: May 24, 2004, 15:14:15 ; Search time 38.6667 Seconds  
(without alignments)  
5027.804 Million cell updates/sec

Title: US-09-806-194A-16  
Perfect score: 3651  
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%	Query					
No.	Score	Match Length	DB	ID			Description

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2	3651	100.0	697	9	US-09-795-847-16	Sequence 16, Appl
3	3651	100.0	697	9	US-09-794-743-16	Sequence 16, Appl
4	3651	100.0	697	9	US-09-794-748-16	Sequence 16, Appl
5	3651	100.0	697	9	US-09-794-925-16	Sequence 16, Appl
6	3651	100.0	697	9	US-09-681-442-16	Sequence 16, Appl
7	3651	100.0	697	10	US-09-869-414-16	Sequence 16, Appl
8	3651	100.0	697	10	US-09-548-366-16	Sequence 16, Appl
9	3651	100.0	697	12	US-10-652-927-16	Sequence 16, Appl
10	3651	100.0	697	12	US-10-652-830-16	Sequence 16, Appl
11	3646	99.9	697	9	US-09-794-927-20	Sequence 20, Appl
12	3646	99.9	697	9	US-09-795-847-20	Sequence 20, Appl
13	3646	99.9	697	9	US-09-794-743-20	Sequence 20, Appl
14	3646	99.9	697	9	US-09-794-748-20	Sequence 20, Appl
15	3646	99.9	697	9	US-09-794-925-20	Sequence 20, Appl
16	3646	99.9	697	9	US-09-681-442-20	Sequence 20, Appl
17	3646	99.9	697	10	US-09-869-414-20	Sequence 20, Appl
18	3646	99.9	697	10	US-09-548-366-20	Sequence 20, Appl
19	3646	99.9	697	12	US-10-652-927-20	Sequence 20, Appl
20	3646	99.9	697	12	US-10-652-830-20	Sequence 20, Appl
21	3643	99.8	697	9	US-09-794-927-18	Sequence 18, Appl
22	3643	99.8	697	9	US-09-795-847-18	Sequence 18, Appl
23	3643	99.8	697	9	US-09-794-743-18	Sequence 18, Appl
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28	3643	99.8	697	10	US-09-548-366-18	Sequence 18, Appl
29	3643	99.8	697	12	US-10-652-927-18	Sequence 18, Appl
30	3643	99.8	697	12	US-10-652-830-18	Sequence 18, Appl
31	3641	99.7	695	9	US-09-794-927-10	Sequence 10, Appl
32	3641	99.7	695	9	US-09-795-847-10	Sequence 10, Appl
33	3641	99.7	695	9	US-09-794-743-10	Sequence 10, Appl
34	3641	99.7	695	9	US-09-794-748-10	Sequence 10, Appl
35	3641	99.7	695	9	US-09-794-925-10	Sequence 10, Appl
36	3641	99.7	695	9	US-09-681-442-10	Sequence 10, Appl
37	3641	99.7	695	9	US-09-149-718-2	Sequence 2, Appli
38	3641	99.7	695	10	US-09-869-414-10	Sequence 10, Appl
39	3641	99.7	695	10	US-09-548-366-10	Sequence 10, Appl
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41	3641	99.7	695	12	US-10-652-927-10	Sequence 10, Appl
42	3641	99.7	695	12	US-10-652-830-10	Sequence 10, Appl
43	3641	99.7	695	14	US-10-169-580-3	Sequence 3, Appli
44	3641	99.7	695	14	US-10-357-935-1	Sequence 1, Appli
45	3641	99.7	695	15	US-10-427-208-45	Sequence 45, Appl

#### ALIGNMENTS

RESULT 1  
 US-09-794-927-16  
 ; Sequence 16, Application US/09794927  
 ; Patent No. US20010016324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gurney, Mark E.

```

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-16

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Query Match          100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-223;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
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Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEOPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV 300
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RESULT 2

US-09-795-847-16

; Sequence 16, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,

AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-795-847-16

Query Match 100.0%; Score 3651; DB 9; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.1e-223;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-794-743-16  
; Sequence 16, Application US/09794743  
; Patent No. US20010021391A1  
; GENERAL INFORMATION:  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Bienkowski, Michael J.  
; APPLICANT: Heinrikson, Robert L.  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Yan, Riqiang  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND  
; TITLE OF INVENTION: USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280BC  
; CURRENT APPLICATION NUMBER: US/09/794,743  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-794-743-16

Query Match 100.0%; Score 3651; DB 9; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.1e-223;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	241	EADDDDEDGEDGDEVEEEAEEPYYEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGEDGDEVEEEAEEPYYEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300



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 Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480  
 |||  
 Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480  
 Qy 481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540  
 |||  
 Db 481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540  
 Qy 541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 |||  
 Db 541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKKQYTSIHHGV 660  
 |||  
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKKQYTSIHHGV 660  
 Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNKK 697  
 |||  
 Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNKK 697

RESULT 4

US-09-794-748-16

; Sequence 16, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-794-748-16

Query Match 100.0%; Score 3651; DB 9; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.1e-223;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 5

US-09-794-925-16

; Sequence 16, Application US/09794925

; Patent No. US20020064819A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280HI

; CURRENT APPLICATION NUMBER: US/09/794,925

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-794-925-16

Query Match 100.0%; Score 3651; DB 9; Length 697;

Best Local Similarity 100.0%; Pred. No. 1.1e-223;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

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Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

|||||

Db 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

|||||

Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy 181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

|||||

Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy 241 EADDDDEDEDGDEVEEEAEOPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTpDAV 300  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 EADDDDEDEDGDEVEEEAEOPYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTpDAV 300  
 Qy 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360  
 Qy 361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420  
 Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA 480  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVA 480  
 Qy 481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540  
 Qy 541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKKQYTSIHHGV 660  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKKQYTSIHHGV 660  
 Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697  
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 Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 6

US-09-681-442-16

; Sequence 16, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681,442

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-681-442-16

Query Match 100.0%; Score 3651; DB 9; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.1e-223;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660



Qy	241	EADDDDEDDGDEVEEEAE EEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDDGDEVEEEAE EEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAENERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK	420
Db	361	QEKVESLEQEAAENERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQONGYENPTYKFFEQM QNKK	697
Db	661	VEVDAAVTPEERHLSKMQONGYENPTYKFFEQM QNKK	697

RESULT 8

US-09-548-366-16

; Sequence 16, Application US/09548366

; Publication No. US20030104365A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES THEREFOR

; FILE REFERENCE: 28341/6280A

; CURRENT APPLICATION NUMBER: US/09/548,366

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-548-366-16

Query Match 100.0%; Score 3651; DB 10; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.1e-223;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHNVQNGKWDSDPSGTK 60
      |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
      |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
      |||
Db    241 EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
      |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
      |||
Db    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480
      |||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy    481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
      |||
Db    481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
      |||
Db    541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMKKKQYTSIHHGV 660
      |||
Db    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMKKKQYTSIHHGV 660

Qy    661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQNKK 697
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|||||  
Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697

RESULT 9  
US-10-652-927-16  
; Sequence 16, Application US/10652927  
; Publication No. US20040043408A1  
; GENERAL INFORMATION:  
; APPLICANT: Gurney et al.  
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor  
and Uses  
; TITLE OF INVENTION: Therefor  
; FILE REFERENCE: 29915/6280N3  
; CURRENT APPLICATION NUMBER: US/10/652,927  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: 09/794,925  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-652-927-16

Query Match 100.0%; Score 3651; DB 12; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.1e-223;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60  
|  
Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60  
  
Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120  
|  
Db 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120  
  
Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180  
|  
Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180  
  
Qy 181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240  
|  
Db 181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240  
  
Qy 241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Db	241	EADDDDEDDGDEVEEEAEPYEEATERTTSIATTTTTTTESVVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA	480
Qy	481	EEIQDEVDELQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNKK	697

RESULT 10

US-10-652-830-16

; Sequence 16, Application US/10652830

; Publication No. US20040048303A1

; GENERAL INFORMATION:

; APPLICANT: Gurney et al.

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses

; TITLE OF INVENTION: Therefor

; FILE REFERENCE: 29915/6280N1

; CURRENT APPLICATION NUMBER: US/10/652,830

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 09/794,925

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-652-830-16

Query Match 100.0%; Score 3651; DB 12; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.1e-223;  
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI PYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVI PYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
        |||
Db    241 EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360
        |||
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLK 420
        |||
Db    361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480
        |||
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVA 480

Qy    481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540
        |||
Db    481 EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSL 540

Qy    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
        |||
Db    541 DDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660
        |||
Db    601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV 660

Qy    661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
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## RESULT 11

US-09-794-927-20

; Sequence 20, Application US/09794927

; Patent No. US20010016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,

AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/794,927

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-794-927-20

Query Match 99.9%; Score 3646; DB 9; Length 697;

Best Local Similarity 99.9%; Pred. No. 2.4e-223;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

```

Qy 241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300  
 |||  
 Db 241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300  
 |||  
 Qy 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360  
 |||  
 Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360  
 |||  
 Qy 361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420  
 |||  
 Db 361 QEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420  
 |||  
 Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480  
 |||  
 Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480  
 |||  
 Qy 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFS 540  
 |||  
 Db 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFS 540  
 |||  
 Qy 541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 |||  
 Db 541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 |||  
 Qy 601 RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITLMLKKKQYTSIHHGV 660  
 |||  
 Db 601 RHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIFITLMLKKKQYTSIHHGV 660  
 |||  
 Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNKK 697  
 |||  
 Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNKK 697  
 |||

RESULT 12

US-09-795-847-20

; Sequence 20, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,

AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 697  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-795-847-20

Query Match 99.9%; Score 3646; DB 9; Length 697;  
Best Local Similarity 99.9%; Pred. No. 2.4e-223;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGV	660

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          |||
Db      601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
          |||
Qy      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
          |||
Db      661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQNKK 697
          |||

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RESULT 13

US-09-794-743-20

; Sequence 20, Application US/09794743

; Patent No. US20010021391A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,

AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280BC

; CURRENT APPLICATION NUMBER: US/09/794,743

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-794-743-20

Query Match 99.9%; Score 3646; DB 9; Length 697;

Best Local Similarity 99.9%; Pred. No. 2.4e-223;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHNVQNGKWDSDPSGTK 60
          |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHNVQNGKWDSDPSGTK 60
          |||
Qy      61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
          |||
Db      61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
          |||
Qy      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMILLPCGIDKFR 180
          |||

```

Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy 181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240  
 |||

Db 181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy 241 EADDDDEDDGDEVEEEAEPEYEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300  
 |||

Db 241 EADDDDEDDGDEVEEEAEPEYEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360  
 |||

Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF 360

Qy 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420  
 |||

Db 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480  
 |||

Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPABA 480

Qy 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNALMPSLTETKTTVELLPVNGEFSL 540  
 |||

Db 481 EEIQDEVDELLQKEQNYSDVLNMISEPRISYGNALMPSLTETKTTVELLPVNGEFSL 540

Qy 541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600  
 |||

Db 541 DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMMLKKQYTSIHHGV 660  
 |||

Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMMLKKQYTSIHHGV 660

Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK 697  
 |||

Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK 697

RESULT 14

US-09-794-748-20

; Sequence 20, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,

AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901



```
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-20
```

```
Query Match          99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.4e-223;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGK 60
        |
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGK 60

Qy     61 TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |
Db     61 TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300
        |
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV 300

Qy    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360
        |
Db    301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHF 360

Qy    361 QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420
        |
Db    361 QEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK 420

Qy    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA 480
        |
Db    421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA 480

Qy    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTTETKTTVELLPVNGEFSL 540
        |
Db    481 EEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTTETKTTVELLPVNGEFSL 540
```



Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVRVPTTAASTPDAV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVA	480
Qy	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Db	481	EEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL	540
Qy	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Db	541	DDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKKQYTSIHHGV	660
Qy	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697
Db	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNKK	697

Search completed: May 24, 2004, 15:28:03  
Job time : 40.6667 secs

OM protein - protein search, using sw model

Run on: May 24, 2004, 15:05:00 ; Search time 37.3333 Seconds  
(without alignments)  
5890.612 Million cell updates/sec

Title: US-09-806-194A-16  
Perfect score: 3651  
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							

---

1	3428	93.9	695	13	Q9DGJ8	Q9dgj8 gallus gall
2	3387	92.8	751	13	Q9DGJ7	Q9dgj7 gallus gall
3	3214	88.0	693	13	Q98SG0	Q98sg0 xenopus lae
4	3190	87.4	695	13	Q98SF9	Q98sf9 xenopus lae
5	3188	87.3	695	13	Q7ZXQ0	Q7zxq0 xenopus lae
6	3103	85.0	747	13	Q91963	Q91963 xenopus. ap
7	2964.5	81.2	699	13	O57394	O57394 narke japon
8	2767.5	75.8	569	13	Q9PVL1	Q9pvl1 gallus gall
9	2613	71.6	534	13	O93296	O93296 gallus gall
10	2567	70.3	678	13	Q7ZZT1	Q7zzt1 brachydanio
11	2529	69.3	738	13	Q90W28	Q90w28 brachydanio
12	2487.5	68.1	694	13	Q8UUR9	Q8uur9 brachydanio
13	2339	64.1	612	13	Q9I9E7	Q9i9e7 brachydanio
14	1928	52.8	384	11	Q8BPC7	Q8bpc7 mus musculu
15	1762	48.3	695	4	Q13861	Q13861 homo sapien
16	1749.5	47.9	669	4	Q14662	Q14662 homo sapien
17	1744	47.8	707	11	Q80US7	Q80us7 mus musculu
18	1740	47.7	695	11	Q64348	Q64348 mus musculu
19	1731	47.4	715	11	Q7TT34	Q7tt34 mus musculu
20	1708	46.8	763	11	Q61482	Q61482 mus musculu
21	1704	46.7	751	11	Q60709	Q60709 mus musculu
22	1655	45.3	472	13	Q8UUS0	Q8uus0 brachydanio
23	1350.5	37.0	357	13	Q8UUI8	Q8uui8 brachydanio
24	1301.5	35.6	522	4	Q9BT36	Q9bt36 homo sapien
25	1090	29.9	218	11	Q8BPV5	Q8bpv5 mus musculu
26	1048.5	28.7	523	4	Q14594	Q14594 homo sapien
27	795	21.8	357	13	Q7ZZT2	Q7zzt2 brachydanio
28	771	21.1	239	13	Q8UUI7	Q8uui7 brachydanio
29	577	15.8	113	13	Q8JH58	Q8jh58 chelydra se
30	561	15.4	182	11	Q9CYS4	Q9cys4 mus musculu
31	478	13.1	97	6	Q28673	Q28673 oryctolagus
32	435.5	11.9	140	13	Q800X9	Q800x9 chelydra se
33	393.5	10.8	82	4	Q16019	Q16019 homo sapien
34	389.5	10.7	82	4	Q16014	Q16014 homo sapien
35	387.5	10.6	82	4	Q16020	Q16020 homo sapien
36	376	10.3	79	11	O35463	O35463 cricetulus
37	358.5	9.8	160	11	Q9QZ78	Q9qz78 cavia sp. p
38	335	9.2	208	11	Q8R0R7	Q8r0r7 mus musculu
39	239	6.5	49	6	O97917	O97917 bos taurus
40	196.5	5.4	727	5	Q95TG7	Q95tg7 drosophila
41	196.5	5.4	5303	5	Q9V628	Q9v628 drosophila
42	193	5.3	785	5	Q9GQ82	Q9gq82 drosophila
43	192.5	5.3	556	5	Q95S93	Q95s93 drosophila
44	192.5	5.3	1110	13	Q91255	Q91255 petromyzon
45	191.5	5.2	556	5	Q9V7I9	Q9v7i9 drosophila

#### ALIGNMENTS

##### RESULT 1

Q9DGJ8

ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.  
AC Q9DGJ8;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Beta-amyloid precursor protein 695 isoform.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sarasa M., Rodolosse A., Sorribas V.;  
RT "Cloning of full-length chicken beta-amyloid precursor protein  
RT isoforms."  
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF289218; AAG00593.1; -.  
DR HSSP; P05067; 1BA4.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR008155; A4\_APP.  
DR InterPro; IPR008154; A4\_extra.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 93.9%; Score 3428; DB 13; Length 695;  
Best Local Similarity 94.0%; Pred. No. 6.6e-198;  
Matches 655; Conservative 17; Mismatches 21; Indels 4; Gaps 3;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCNHGHPIVVPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCEKSMNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEDDSVWVGADTDYADGSEDKVVE--VAEEEEVAEVE	238
Db	181	GVEFVCCPLAEESDNLDSADAEDDSVWVGADADYADGSDDKVVEEQPEEDEELTVVE	240
Qy	239	EEEADDDDEDEDGDEVEEEAEPYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASPD	298
		:  :        :	
Db	241	DEDADDD-DDDDGDEI-EETEEYEEATERTTSIATTTTTTTTESVEEVVRVPTTAASPD	298
Qy	299	AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ	358
Db	299	AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ	358
Qy	359	HFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRRLALENYITALQAVPPRPRHVFNM	418
Db	359	HFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRRIALENYITALQTVPPRPRHVFNM	418

Qy 419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPA 478  
 |||  
 Db 419 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPA 478  
 Qy 479 VAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTVELLPVNGEF 538  
 |||:|  
 Db 479 VAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTETKTVELLPVDGEF 538  
 Qy 539 SLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA 598  
 |||:|  
 Db 539 SLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVSEVKMDA 598  
 Qy 599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658  
 |||  
 Db 599 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH 658  
 Qy 659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695  
 |||  
 Db 659 GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN 695

## RESULT 2

### Q9DGJ7

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.  
 AC Q9DGJ7;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Beta-amyloid precursor protein 751 isoform.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sarasa M., Rodolosse A., Sorribas V.;  
 RT "Cloning of full-length chicken beta-amyloid precursor protein  
 RT isoforms.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF289219; AAG00594.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
KW Protease inhibitor; Serine protease inhibitor.  
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 92.8%; Score 3387; DB 13; Length 751;  
Best Local Similarity 86.9%; Pred. No. 2.1e-195;  
Matches 654; Conservative 18; Mismatches 21; Indels 60; Gaps 4;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLMHMNVQNGKWESDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNHGHPIVVPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMMLPCGIDKFR 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMMLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWGGADTDYADGSEDKVVE--VAEEEEVAEVE 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 GVEFVCCPLAEESDNLDSADAEDDDSDVWGGADADYADGSDDKVVEEQPEEDEELTVVE 240

Qy    239 EEEADDDDEDEDGDEVEEEAEPEYEATERTTTSIATTTTTTTTESVEEVVR----- 288
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 DEDADDD-DDDDGDEI-EETEEFYEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETG 298

Qy    289 -----VPTTAASTPDAVDK 302
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    299 PCRAMISRWFYDVAEGKCAPFFYGGCGGNRNNFDSEEYCMVCGSVLPPTAASTPDAVDK 358

Qy    303 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHFQE 362
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    359 YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHFQE 418

Qy    363 KVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKY 422
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    419 KVESLEQEAANERQQLVETHMARVEAMLNDRRIAENYITALQTVPPRPRHVFNMLKKY 478

Qy    423 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVAEAE 482
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    479 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLFLYNVPVAEAE 538

Qy    483 IQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFLDD 542
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    539 IQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTETKTTVELLPVDGEFLDD 598

Qy    543 LQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRH 602
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    599 LQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTTEEVSVKMDAEFRH 658

Qy    603 DSGYEVVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 662
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```



Db 659 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGCVVE 718

Qy 663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695  
 ||| : ||:| | |||| || ||||| : ||||| : ||| |||

Db 719 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 751

RESULT 3

Q98SG0

ID Q98SG0 PRELIMINARY; PRT; 693 AA.  
 AC Q98SG0;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Beta-amyloid precursor protein A.  
 GN APP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Van den Hurk W.H.;  
 RL Thesis (2001), Department of Biological Sciences,  
 RL University of Nijmegen, Nijmegen, Netherlands.  
 DR EMBL; AJ298150; CAC37193.1; -.  
 DR HSSP; P05067; 1HZ3.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 KW Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match 88.0%; Score 3214; DB 13; Length 693;  
 Best Local Similarity 87.8%; Pred. No. 4.8e-185;  
 Matches 612; Conservative 36; Mismatches 43; Indels 6; Gaps 4;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60  
 ||| : ||:| | |||| || ||||| : ||||| : ||| |||

Db 1 MLPHITLLVLTG-GALALEVPADGNGLLAEPQIAMFCGKLNHMNMNVQNGKWETDVSGTK 59

Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120  
 || ||||| : ||||| : | | : |||||

Db 60 GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy 121 EKVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180  
 ||||| : ||||| : |||| : ||: |||||

Db 120 EKVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKSMMLHEYGMLLPCGIDKFR 179



DR EMBL; AJ298151; CAC37194.1; -.  
 DR HSSP; P05067; 1HZ3.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 KW Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;

Query Match 87.4%; Score 3190; DB 13; Length 695;  
 Best Local Similarity 87.2%; Pred. No. 1.3e-183;  
 Matches 609; Conservative 39; Mismatches 44; Indels 6; Gaps 5;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
		:   :                            :             :	
Db	1	MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVS GTK	59
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
		:       :     :	
Db	60	GCIGTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG	119
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
		:       :     :	
Db	120	EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR	179
Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEV--AEEEEVAEVE	238
		:                         :	
Db	180	GVEFVCCPTAEESSESFDSADA-EDSDVWWGGADADYVDRSDDKAVEAQPEEEEEVVEVE	238
Qy	239	EEEADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVR-VPTTAASTP	297
		:	
Db	239	EEEADDD-DEDDGDETEEEPEEPYEEATERTTSIATTTTTTTTESVEEVVRVAVPATAVSTP	297
Qy	298	DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVI	357
		:    :    :	
Db	298	DAVDKYLENPNDENEHDFLKAKEKLEGGHREKMSQVMKEWEEAERQAKNLPKADKKAVI	357
Qy	358	QHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFN	417
		:	
Db	358	QHFQEKVESLEQEAAANERQQLVETHMARVEATLNDRRRIALENYITALQADPPRPRHVFN	417
Qy	418	MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVP	477
Db	418	MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVP	477
Qy	478	AVAEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLMPSLTETKTTVELLPVNGE	537
		:    :    :    :             :	
Db	478	AVAEIQDEVDELQKEQNYSDVMVSNMVS DHRVSYGNLMPSLSETKTTVELLPVDGE	537
Qy	538	FSLDDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEISEVKMD	597

[illegible]

07ZX00

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ID      Q7ZXQ0      PRELIMINARY;      PRT;      695 AA.
AC      Q7ZXQ0;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RA      Klein S., Strausberg R.;
RL      Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC044324; AAH44324.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
KW      Hypothetical protein.
SQ      SEQUENCE      695 AA;  78803 MW;  C1BD8AACC3356B05 CRC64;

```

Query Match 87.3%; Score 3188; DB 13; Length 695;  
Best Local Similarity 87.2%; Pred. No. 1.8e-183;  
Matches 609; Conservative 38; Mismatches 45; Indels 6; Gaps 5;

```

Qy      1  MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK 60
      ||| : ||| | | |||| || ||||| ||||| : ||||| ||||| : | |||
Db      1  MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLLNMHMNVQNGKWETDVSGTK 59

Qy     61  TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      || ||||| ||||| ||||| ||||| ||||| : ||||| : | : |||||
Db     60  GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119

Qy    121  EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

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Db      120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR 179
QY      181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEV--AEEEEVAEVE 238
Db      180 GVEFVCCPTAEESSEFSDADA-EDDSVWWGGADADYVDRSDDKAVEAQPEEEEEVEVE 238
QY      239 EEEADDDDEDEDGDEVEEEAEEPYYEATERTTSIATTTTTTTESVEEVVR-VPTTAASTP 297
Db      239 EEEADDD-DDDDGDETEEEPEEPYYEATERTTSIATTTTTTTESVEEVVRVAVPATAVSTP 297
QY      298 DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVI 357
Db      298 DAVDKYLENPNDENEHDFLKAKEKLEKHEKREKMSVMEKEWEEAERQAKNLPKADKKAVI 357
QY      358 QHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRRLALENYITALQAVPPRPRHVFN 417
Db      358 QHFQEKVESLEQEAAKERQQLVETHMARVEATLNDRRRIALENYITALQADPPRPRHVFN 417
QY      418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
Db      418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVP 477
QY      478 AVAAEIQDEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGE 537
Db      478 AVAAEIQDEVDELFOKEQNYSDMVSNMVSDHRVSYGNDAIMPSTETKTTVELLPVDGE 537
QY      538 FSLDDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMD 597
Db      538 FNVEDLQPWHSFGVDSVPANTENEVEPVDPARPAADRGLTTRPGSGLTNIKREEISEVKMD 597
QY      598 AEFRHDSGYEVHHQKLVEFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH 657
Db      598 SEYRHDAAYEVHHQKLVEFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIH 657
QY      658 HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db      658 HGVVEVDAAVTPEERHLTKMQQNGYENPTYKFFEQMQN 695

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RESULT 6

Q91963

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ID      Q91963          PRELIMINARY;          PRT;      747 AA.
AC      Q91963;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      APP747.
GN      APP747.
OS      Xenopus.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC      Xenopodinae.
OX      NCBI_TaxID=8353;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93129227; PubMed=1282805;

```

RA Okado H., Okamoto H.;  
 RT "A Xenopus homologue of the human beta-amyloid precursor protein:  
 RT developmental regulation of its gene expression.";  
 RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).  
 DR EMBL; S52417; AAB24853.1; -.  
 DR HSSP; P05067; 1HZ3.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Protease inhibitor; Serine protease inhibitor.  
 SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 85.0%; Score 3103; DB 13; Length 747;  
 Best Local Similarity 81.0%; Pred. No. 2.5e-178;  
 Matches 598; Conservative 35; Mismatches 41; Indels 64; Gaps 5;

Qy	17	ALEVPTDGNAGLLAEPQIAMF-CGR_LNMHMNVQNGKWDSPSGTKTCIDTKEGILQYCQE	75
Db	15	ALEVLVDGNGGLLAEPQIAMFVSAR_LNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE	71
Qy	76	VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEEFVSDALLVPDKCKF	135
Db	72	VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEEFVSDALLVPDKCKF	131
Qy	136	LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGM_LPCGIDKFRGVEFVCCPLAEESDN	195
Db	132	LHQERMDICETHLHWHTVAKESCSEKSM_SLEHYGM_LPCGIDKFRGVEFVCCPSAEES	191
Qy	196	VDSADAEEDSDVWVGADTDYADGSEDKVVEVA---EEEEVAEEEEEEADDEDDEDGDE	253
Db	192	FDSADAAEDDCDVWVGADADYVDRSDDKAVEAQPD_EEEVVEVEEEETDDDED--DGDE	249
Qy	254	VEEEAEPEPYEEATERTTTSIATTTTTTTTTSVEEVVR-----	288
Db	250	AEEPEPEPYEEATERTTTSIATTTTTTTTTSVEEVVREVCSEQAETGPCRAMISRWYYDVTE	309
Qy	289	-----VPTTAASTPDAVDKYLET_PGDENEHAHFQ	317
		:	
Db	310	SKCAQFIYGGCGGNRNNFESDDYCMVAVCGSVIPATAASTPDAVDKYLENPN_DENEHDFL	369
Qy	318	KAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEAA_NERQQ	377
Db	370	KAKERLEGKHREKMSEVMKEWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEAAKQRQQ	429

Qy	378	LVETHMARVEAMLNDRRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHf	437
Db	430	LVETHMARVEAMLNDRRRRIALENYITALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHf	489
Qy	438	EHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLOKEQNY	497
Db	490	EHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPAAVEEIQDEVDELFOKEQNY	549
Qy	498	SDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLLDQLPWHFSFGADSVPAN	557
Db	550	SDDMVSNMVS DHRVSYGNDALMPSLSETKTTVELLPVDGEFNIEDLQPVHFSFGVDSVPAN	609
Qy	558	TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFA	617
Db	610	TENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDSEYRHD TAYEVHHQKLVFFA	669
Qy	618	EDVGSNKGAIIGLMVGGVVIATVIVITLVLMLKKKQYTSIHGGVVEVDAAVTPEERHLSKM	677
Db	670	EEVGSNKGAIIGLMVGGVVIATVIVITLVLMLKKKQYTTIHGGVVEVDAAVTPEERHLTKM	729
Qy	678	QQNGYENPTYKFFEQMQN	695
Db	730	QQNGYENPTYKFFEQMQN	747

DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
SQ SEQUENCE 699 AA; 78879 MW; 952915C309D50E5C CRC64;

Query Match 81.2%; Score 2964.5; DB 13; Length 699;  
Best Local Similarity 80.8%; Pred. No. 4.9e-170;  
Matches 569; Conservative 58; Mismatches 58; Indels 19; Gaps 8;

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Qy      2 LPG-LALLLLAAWTA-----RALEVPTDGNAGLL-AEPQIAMFCGRLNMHMNVQNGKW 52
      ||| | :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      5 LPGRLGMLLLAAAAALVLAPLCRALEVPTDGGAGLLAAEPQIAMFCGKLNMHVNVQTGKW 64

Qy     53 DSDPSGKTCTIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFV 112
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     65 VSDPSGTNTCFGTKEGILRYCQEVYPDLQITNVVEANQPITIQNWCKKGRKQCKGHPHIV 124

Qy    113 IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLL 172
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    125 VPYRCLVGEFVSDALLVPDKCKFLHREKMDTCESHLVWHTVAKETCGDKIMNLHDYGMLL 184

Qy    173 PCGIDKFRGVFEVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEE 232
      ||||| :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db    185 PCGIDEFRGVFEVCCPIPEENDKIDS-DMDEEDSDVWWGGDDADYADGG-DKTV-----EE 238

Qy    233 EVAEVEEEEEADDDDEDDGDEVEEEE-AEPEYEEATERTTSIATTTTTTTESVEEVVRVPT 291
      : | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db    239 KPIEEEEEEDESDDIDDDDDLDDEVVEDQYEDPTEHTTS---STTTTTEAIEEVVRVPT 295

Qy    292 TAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKA 351
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    296 TAASTPDAVDKYLETPGDENEHAYFQKAKERLEAKHRERMSKIMREWEEAERQAKNLPKA 355

Qy    352 DKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRRLALENYITALQAVPPR 411
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    356 DKKAVIQRFQEMVESLEQEAAASERQQLVETHMARVEAMLNDRRRRLALENYLAALQADPPR 415

Qy    412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 471
      |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    416 PRHVLNALKKYSRAEQKDRQHTLKHFDHVRVDPEKAAQIKSQVMTHLHVIDERMNQSL 475

Qy    472 LLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTLTETKTVEL 531
      || | | :| | | | | | | | | | | | | | | | | | | | | | | |
Db    476 LLYKVPVAAVEEIQDEVDELLQREERSYMDDMMANSVSDTRISYGNDAIVPSLSETKTIEL 535

Qy    532 LPVNGEFSLDDLQPDWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEI 591
      || :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db    536 LPDDGEFILDDLQPPHPFVIESIPANTENEVEPVDPARPAPDRGLTTRPGSGLTGKITEEI 595

Qy    592 SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKK 651
      :| :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db    596 AELKMETEFQQDSGYEVHHQKLVFVFPKDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKK 655

Qy    652 QYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
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Q9PVL1

Query Match 75.8%; Score 2767.5; DB 13; Length 569;  
Best Local Similarity 93.5%; Pred. No. 2.6e-158;  
Matches 535; Conservative 14; Mismatches 18; Indels 5; Gaps 4;

Qy	126	ALLVPDKCKFLHQERMDVCE	THLHWHTVAKETCSEKSTN	LHDYGMLLPCGIDKFRGVEFV	185
			:		
Db	1	ALLVPDKCKLLHQERMDVCE	THLHWHTVAKESCSEKSMN	LHDYGMLLSCGIDKFRGVEFV	60
Qy	186	CCPLAEESDNVDSADAEE	DDSDVWVGADTDYADGSE	DKVVE--VAEEEEVAEEEE	243
		:    :		:	
Db	61	CCPLAEESDNLDSADAEE	DDSDVWVGADADYADGS	DDKVVEEQPEEDEELTV	120
				VEDEDAD	
Qy	244	DDEDDDEDGDEVEEEAE	EPYEEATERTT	SIATTTTTTTESVEEV	303
		:	:		
Db	121	DD-DDDDGDEI-EETEE	EYEEATERTT	SIATTTTTTTESVEEV	178
				RVPTTAASTPDVVDKY	
Qy	304	LETPGDENEHAHFQKA	KERLEAKHRERMSQVM	REWEEAERQAKNLPKA	363
Db	179	LETPGDENEHAHFQKA	KERLEAKHRERMSQVM	REWEEAERQAKNLPKA	238
				DKKAVIQHFQEK	

QY 364 VESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYV 423  
 |||:|||||  
 Db 239 VESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITALQTVPPRPRHVFNMLKKYV 298  
 QY 424 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVAEEI 483  
 |||:|||||  
 Db 299 RAEQKDRQHTLKHFEHVRMVDPKKAVQIRSQVMTHLRVIYERMNQSLSLFLYNPAVAEEI 358  
 QY 484 QDEVDELLQKEQNYSDVLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEFSLDDL 543  
 |||:|||||  
 Db 359 QDEVDELLQKEQNYSDVLANMISEPRI SYGNDALMPTLTETKTTVELLPVVG EFSLDDL 418  
 QY 544 QPWHSGFADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHD 603  
 |||||:|:|  
 Db 419 QPWHSPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTEEVS EVKMDAEFRHD 478  
 QY 604 SGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHG VVEV 663  
 |||:|||||  
 Db 479 SGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIANVIVITLVMLKKKQYTSIHG VVEV 538  
 QY 664 DAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695  
 |||||  
 Db 539 DAAVTP-ERHLSKMQQNGYENPTYKFFEQMQN 569

# RESULT 9

O93296

ID O93296 PRELIMINARY; PRT; 534 AA.  
 AC O93296;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Amyloid protein (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98337885; PubMed=9671674;  
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
 RA Milligan C.E.;  
 RT "Increased production of amyloid precursor protein provides a  
 RT substrate for caspase-3 in dying motoneurons."  
 RL J. Neurosci. 18:5869-5880(1998).  
 DR EMBL; AF042098; AAC25052.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.

DR PROSITE; PS00320; A4\_INTRA; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 71.6%; Score 2613; DB 13; Length 534;  
Best Local Similarity 94.8%; Pred. No. 4.7e-149;  
Matches 506; Conservative 13; Mismatches 11; Indels 4; Gaps 3;

```
Qy      164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSED 223
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      3   NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNLDSADAEDDDSDVWVGADADYADGSDD 62

Qy      224 KVVE--VAEEEEVAEVEEEEEADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTE 281
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:|||||
Db      63 KVVEEQPEEDEELTVVEDEDADDD-DDDDGDEI-EETEEYEEATERTTSIATTTTTTTE 120

Qy      282 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 341
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 SVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEA 180

Qy      342 ERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRRLALENY 401
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      181 ERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRRIALENY 240

Qy      402 ITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 461
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      241 ITALQTVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRV 300

Qy      462 IYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPS 521
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      301 IYERMNQSLSFLYNVPAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPS 360

Qy      522 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGS 581
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      361 LTETKTTVELLPVDGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGS 420

Qy      582 GLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 641
          ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      421 GLTNVKTEEIVSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 480

Qy      642 VITLVMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      481 VITLVMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 534
```

RESULT 10

Q7ZZT1

ID Q7ZZT1 PRELIMINARY; PRT; 678 AA.

AC Q7ZZT1;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Amyloid protein a variant 2.

GN APPA.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Groth C., Lardelli M.;  
 RT "Investigation of zebrafish appa expression during embryogenesis."  
 RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY271746; AAP22958.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 678 AA; 76755 MW; 94163778444FD0BC CRC64;

Query Match 70.3%; Score 2567; DB 13; Length 678;  
 Best Local Similarity 72.0%; Pred. No. 3.7e-146;  
 Matches 499; Conservative 78; Mismatches 94; Indels 22; Gaps 11;

Qy	5	LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGKTCTCID	64
		:  :  :  :  :                :    :  :  :  :  :  :  :	
Db	6	LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPPDPSGSKSCIG	65
Qy	65	TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVS	124
		:  :    :       :      :	
Db	66	NKEGILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVS	125
Qy	125	DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF	184
		:   :          :  :               :	
Db	126	DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF	185
Qy	185	VCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAVEEEEEADD	244
		: :               :    :   : :       :   :	
Db	186	VCCP-ADAGKESESAAVEEDSDVWWGGAEDYTENSMTTR--DAAAEPAV--LEDDEDAD	240
Qy	245	DEDDDEDGD-EVEEEAEPEYEEATERTT-SIATTTTTTTSVEEVVRVPTTAASTPDAVDK	302
		:  :      : :           :   : : :             :         :	
Db	241	EEDEDGDGRDEKIEEEEEERTQSTSAAALTSTTTTTSVEEVVRVPTPSSSPDPAVDR	300
Qy	303	YLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQE	362
		:    :	
Db	301	YLETPADENEHAHFLKAKESLETKHRERMSQVMREWEAAERQAKSLPRNDKKAVIQHFQE	360
Qy	363	KVESLEQEAAENERQQQLVETHMARVEAMLNDRRRRLALENYITALQAVPPRPRHVFNMLKKY	422
		:    :  :                :          :    :          :	
Db	361	KVEALEQESASERQQQLVETHMARVEALLNDRRRRLALESYLSALQADPPRPRHVFSLKKY	420
Qy	423	VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMNQSLSLLYNVPVAEE	482
Db	421	VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSGLLLYKVPGVADD	480
Qy	483	IQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTLTETKTTVELLPVNGEFSLDD	542

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      |||:| |||:| | |||: |: |:| ||| ||| | :|||
Db      481 IQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFGF 536
Qy      543 LQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRH 602
      : | || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      537 IHP-ESFN----QPNTHNQVEPVDARVPDLDLATRPVSGL---KPDDIPELRMEAEERH 588
Qy      603 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 662
      ||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      589 S---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIVITLVMLRKKQYTSIHGGIIE 645
Qy      663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      646 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 678

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RESULT 11

Q90W28

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ID   Q90W28          PRELIMINARY;          PRT;   738 AA.
AC   Q90W28;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid precursor protein.
GN   APPA OR APP.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Expression analysis of zebrafish app.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF389401; AAK64495.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE 738 AA; 83577 MW; AF480F6D308FD298 CRC64;

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Query Match 69.3%; Score 2529; DB 13; Length 738;  
Best Local Similarity 66.4%; Pred. No. 8e-144;  
Matches 501; Conservative 79; Mismatches 90; Indels 84; Gaps 14;

Qy	5	LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGKTCID	64
		:  :  :   :  :                  :      :  :    :       :	
Db	6	LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLLNMHINIQSGKWEPDPSGSKSCIG	65
Qy	65	TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVGEFVS	124
		:    :      :    :	
Db	66	NKEGILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVS	125
Qy	125	DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF	184
		:  :                  :	
Db	126	DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF	185
Qy	185	VCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEEADD	244
		: :                 :     :   :       :  :  :  :	
Db	186	VCCP-ADAGKESESAAVEEDSDVWWGGAEADYTENSMTR--DAAAEPAVLE-DDEDADE	241
Qy	245	DED-DEDGD-----EVEEEAEEPVEEATERTT-SIATTTTTTTESVEEVVR-----	288
		:      :      :              :  :  :  :	
Db	242	EEDEDQDGDGRDEKIEEEEE--EERTQSTSAALTSTTTTTTESVEEVREVCFASAET	299
Qy	289	-----VPTTAASTPDAVD	301
		:    :	
Db	300	GPCRAMLSRWYYVREERRCAPFIYGGCGGNRNNFEESEYCLSVCSGVLPTPSSSPDAVD	359
Qy	302	KYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQ	361
		:                                    :  :	
Db	360	RYLETPADENEHAHFLKAKESLETKHRERMSQVMREWEAAERQAKSLPRNDKKAVIQHFQ	419
Qy	362	EKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKK	421
		:      :  :                :            :  :	
Db	420	EKVEALEQESASERQQLVETHMARVEALNDRRLALESYLSALQADPPRPRHVFSLKK	479
Qy	422	YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPVAE	481
		:                        :	
Db	480	YVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVAD	539
Qy	482	EIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLD	541
		:    :          :          :  :                :	
Db	540	DIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---AGLELLPAEDTQGFG	595
Qy	542	DLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFR	601
		:                     :                      :  :  :  :	
Db	596	FIHP-ESFN----QPNTHNQVEPVDARPVPLDLATRPVSGL---KPDDIPELRMEAEER	647
Qy	602	HDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVV	661
		:                            :          :          :	
Db	648	HS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIIVITLVMLRKKQYTSIHGGII	704
Qy	662	EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
Db	705	EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN	738

RESULT 12

Q8UUR9

ID Q8UUR9 PRELIMINARY; PRT; 694 AA.  
 AC Q8UUR9;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Putative membrane protein.  
 GN APPB.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX PubMed=11862463;  
 RA Musa A., Lehrach H., Russo V.E.A.;  
 RT "Distinct expression patterns of two zebrafish homologues of the human  
 RT APP gene during embryonic development.";  
 RL Dev. Genes Evol. 211:563-567(2001).  
 DR EMBL; AJ315639; CAC85736.1; -.  
 DR ZFIN; ZDB-GENE-020220-1; appb.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 694 AA; 79228 MW; 2B03382D411162DC CRC64;

Query Match 68.1%; Score 2487.5; DB 13; Length 694;  
 Best Local Similarity 67.9%; Pred. No. 2.3e-141;  
 Matches 477; Conservative 98; Mismatches 97; Indels 31; Gaps 9;

Qy	7	LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRINMNMVQNGKWDSDPSGKTCTCIDTK	66
		: : : : :  :          :        :      :    :    :	
Db	9	LLMLTTLTLAIEVPSDDSVGLLAEPQVAMFCGKLNHINVQSGKWEPTGTGKSCISTK	68
Qy	67	EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA	126
		:          :	
Db	69	EGILKYCQEVYPDLQITNVVEANQPVSINQWCKMGRRCRSHTHIVVPYRCLVGEFVSDA	128
Qy	127	LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC	186
		:  :              :  :	
Db	129	LLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVC	188
Qy	187	CPLAEESDNVDSADAEEEDSDVWWGGADTDYADGS--EDKVV-----EVAEEEEVAEVEE	239
		:  :  :  :  :  :          :  :      :  :  :  :  :  :  :	
Db	189	CPMEEQKD-LDSEEQEEANSVWWGGAETETDASVLKEQVTAKPDPVTEDEDLNNEE	247

Qy	240	EEADDDDEDDGDGEVEEEAAEE-----PYEEATERTTTIA--TTTTTTTESVEEVRVPTT	292
Db	248	EEVWDNDEDDGDGEDDEDEEDDDEDIIDEQDTSEQTSNIAMTTTTTTTTTESIEEVRVPTM	307
Qy	293	AASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKAD	352
Db	308	APSPADAVDRYLEAPGDMNEHMRFAQKAKESLEAKHREKMSEVMREWEAAERQAKNLPKAD	367
Qy	353	KKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRRLALENYITALQAVPPRP	412
Db	368	KKTIIQRFQEKVESLEKEAAGERQQLVETHMARVEALLNDRRRQALESYLSSLQSDQPRP	427
Qy	413	RHVFENMLKKYVRAEQKDRQHTLKHFEHVVMVDPKKAQIRSQVMTHLRVIYERMNQSLSL	472
Db	428	RQVLNLLKKYIRAEQKDRQHTLKHFEHVREVDPKKASQIRPFVMTHLRVIEERMNQSLSL	487
Qy	473	LYNVPAAVEEIQDEVDLQKEQNYSDDLANMISEPRISYGNDAIMPSTETKTTVELL	532
Db	488	LYKVPQVANDIQDQVAVLVQRDQAEVTQQLSSLQSKMRVSYGNDAIMPDLDPDSTPLDNL	547
Qy	533	PVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEIS	592
Db	548	PPEQD-GLGFIHP-ESFN----QANTDNHVEPVDARPIPERGLPTRP-----EIP	591
Qy	593	EVKMDAEFRHDSGYEVHHQKLVFVFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMKKKQ	652
Db	592	KVRLDIEERHNAGYDVRDKRLMFLAEDMGSNKGAIIGLMVGGVVIATVIVITLVMKKKQ	651
Qy	653	YTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
Db	652	YTSIHGGVIEVDAAVTPEERHLAKMQQNGYENPTYKFFEQMQN	694





RESULT 14

Q8BPC7

ID Q8BPC7 PRELIMINARY; PRT; 384 AA.  
 AC Q8BPC7;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Amyloid beta (Fragment).  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK076506; BAC36369.1; -.  
 DR MGD; MGI:88059; App.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;

Query Match 52.8%; Score 1928; DB 11; Length 384;  
 Best Local Similarity 98.2%; Pred. No. 4.7e-108;  
 Matches 377; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 312 EHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEA 371  
 |||  
 Db 1 EHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEA 60  
 Qy 372 ANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLKKYVRAEQKDRQ 431  
 |||  
 Db 61 ANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLKKYVRAEQKDRQ 120  
 Qy 432 HTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELL 491  
 |||  
 Db 121 HTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELL 180  
 Qy 492 QKEQNYSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSLLDLQPWHSFGA 551  
 |||:|||||  
 Db 181 QKEQNHSDVLNMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSLLDLQPWHPFGV 240  
 Qy 552 DSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQ 611  
 |||:|||||

```

Db          241 DSVPA NTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFGHDSGFEVRHQ 300
Qy          612 KLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHG VVEVDAAVTPEE 671
              |||
Db          301 KLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHG VVEVDAAVTPEE 360
Qy          672 RHL SKMQQNGYENPTYKFFEQMQN 695
              |||
Db          361 RHL SKMQQNGYENPTYKFFEQMQN 384

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RESULT 15

Q13861

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ID   Q13861          PRELIMINARY;          PRT;          695 AA.
AC   Q13861;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Binding protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Vostrov A.A., Quitschke W.W., Schwarzman A.L., Blangy A., Cuzin F.,
RA   Wesley U.V., Hagag N.G., Goldgaber D.;
RT   "Cloning of a protein that binds to a recognition sequence in the APP
RT   promoter.";
RL   Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L19597; AAA35601.1; -.
DR   HSSP; P05067; 1MWP.
DR   InterPro; IPR008155; A4 APP.
DR   InterPro; IPR008154; A4_extra.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER      1      1
FT   NON_TER      695    695
SQ   SEQUENCE      695 AA; 79238 MW; 728CA8ACBB7594FB CRC64;

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Query Match          48.3%; Score 1762; DB 4; Length 695;
Best Local Similarity 50.8%; Pred. No. 9.7e-98;
Matches 366; Conservative 113; Mismatches 171; Indels 70; Gaps 17;

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Qy          5  LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
              | |||  || || :      |||  : ||| ||||| : ||| : ||| : ||
Db          15  LLLLLLVGLTAPALALAGYIEALANAGTGFVAEPAEPQIAMFCGKLNMHVNIQTGKWE PDP 74
Qy          57  SGTKT CIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
              : ||| : | : ||| : ||||| : ||||| : ||| | : | ||| : | || : |
Db          75  TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQVRSIDNWCRRDKKQCKS--RFVTPFK 132
Qy          117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGM LLLPCGI 176

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Db	133	:   :   :               :   :           :	CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHTVVKEACLTQGMTLYSYGMLLPCGV	192
Qy	177		DKFRGVFEVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE	236
Db	193	:       :       : :   :     :   :   :   :   :	DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-----EEEEDEEEDYDVYKSEFPTEAD	245
Qy	237		VEE--EEA--DDDEDEDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTESVE	284
Db	246	:   :     :       :   :     : :         :   : : :	LEDFTAAVDEDEDEEEGEEVVEDRDYDYDTFKGDDYNE--ENPTEPGSDGTMSDKEIT	303
Qy	285		EVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQ	344
Db	304	:                               :         :   :	HDVKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQ	362
Qy	345		AKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITA	404
Db	363	: : : :           :   :       :           :         :	AKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRMALENYLAA	422
Qy	405		LQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE	464
Db	423	:       :   :                 :   :           :	LQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEE	482
Qy	465		RMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTE	524
Db	483	:   :   :   :   :   :   :   :   :	RRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTASISE	525
Qy	525		TKTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGL-----	575
Db	526	:     : :   :                   :	TPVDVR---VSSEES-EEIPPFHPF--HPFPALPENEGSGVGEQ---DGGLIGAEKVIN	576
Qy	576		-TTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG	634
Db	577	: : :   : :   : :         : :     :   :	SKNKVDENMVIDETLDVKEMIFNAE--RVGGLEERESVGPLREDFSLSSSALIGLLVIA	634
Qy	635		VVIATVIVITLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMQ	694
Db	635	:       :   :   :     :         :       :         :	VAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHYENPTYKYLEQQMQ	694

Search completed: May 24, 2004, 15:14:05  
Job time : 40.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2004, 15:02:24 ; Search time 10.3333 Seconds  
(without alignments)  
3512.216 Million cell updates/sec

Title: US-09-806-194A-16  
Perfect score: 3651  
Sequence: 1 MLPGLALLLLAAWTARALEV.....QQNGYENPTYKFFEQMQNKK 697

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3590.5	98.3	770	1	A4_HUMAN	P05067	h amyloid b
2	3590.5	98.3	770	1	A4_MACFA	P53601	m amyloid b
3	3584	98.2	751	1	A4_SAISS	Q95241	s amyloid b
4	3535.5	96.8	770	1	A4_PIG	P79307	s amyloid b
5	3522.5	96.5	770	1	A4_CAVPO	Q60495	c amyloid b
6	3493.5	95.7	770	1	A4_MOUSE	P12023	m amyloid b
7	3493.5	95.7	770	1	A4_RAT	P08592	r amyloid b
8	2573	70.5	780	1	A4_TETFL	O73683	tetraodon f
9	2448.5	67.1	737	1	A4_FUGRU	O93279	fugu rubrip
10	1735	47.5	695	1	APP2_MOUSE	Q06335	mus musculu
11	1728	47.3	763	1	APP2_HUMAN	Q06481	homo sapien
12	1716	47.0	765	1	APP2_RAT	P15943	rattus norv
13	1190	32.6	650	1	APP1_HUMAN	P51693	homo sapien
14	1185	32.5	653	1	APP1_MOUSE	Q03157	mus musculu
15	817.5	22.4	686	1	A4_CAEEL	Q10651	caenorhabdi
16	748.5	20.5	887	1	A4_DROME	P14599	drosophila
17	292	8.0	59	1	A4_BOVIN	Q28053	bos taurus

18	288	7.9	58	1	A4_RABIT	Q28748	oryctolagus
19	288	7.9	58	1	A4_SHEEP	Q28757	ovis aries
20	287	7.9	58	1	A4_CANFA	Q28280	canis famil
21	283	7.8	57	1	A4_URSMA	Q29149	ursus marit
22	185.5	5.1	407	1	IE68_HSVSA	Q01042	herpesvirus
23	185.5	5.1	993	1	SCP1_MOUSE	Q62209	mus musculu
24	176	4.8	2004	1	MYS3_HUMAN	Q92794	homo sapien
25	175.5	4.8	802	1	NAB3_YEAST	P38996	saccharomyc
26	173.5	4.8	793	1	CALD_HUMAN	Q05682	homo sapien
27	172	4.7	771	1	CALD_CHICK	P12957	gallus gall
28	172	4.7	1498	1	GOA3_HUMAN	Q08378	homo sapien
29	169.5	4.6	297	1	TRT2_HUMAN	P45379	homo sapien
30	169.5	4.6	721	1	YCF2_OENPI	P31568	oenothera p
31	168.5	4.6	1875	1	MLP1_YEAST	Q02455	saccharomyc
32	168	4.6	1240	1	YNJ1_YEAST	P53935	saccharomyc
33	167.5	4.6	1976	1	MYHA_HUMAN	P35580	homo sapien
34	166.5	4.6	816	1	YG3A_YEAST	P53278	saccharomyc
35	166.5	4.6	1976	1	MYHA_RAT	Q9jlt0	rattus norv
36	164.5	4.5	1447	1	GOA3_MOUSE	P55937	mus musculu
37	163.5	4.5	681	1	MP10_HUMAN	O00566	homo sapien
38	163	4.5	2017	1	MYSN_DROME	Q99323	drosophila
39	162.5	4.5	712	1	NUCL_RAT	P13383	rattus norv
40	160.5	4.4	1976	1	MYHA_BOVIN	Q27991	bos taurus
41	160	4.4	694	1	NUCL_CHICK	P15771	gallus gall
42	159.5	4.4	1955	1	PUMA_PARUN	O61308	parascaris
43	158	4.3	301	1	TRT2_CHICK	P02642	gallus gall
44	157.5	4.3	706	1	NUCL_HUMAN	P19338	homo sapien
45	156.5	4.3	1332	1	SPT7_YEAST	P35177	saccharomyc

# ALIGNMENTS

## RESULT 1

### A4\_HUMAN

ID A4\_HUMAN STANDARD; PRT; 770 AA.  
AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;  
AC Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease  
DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-  
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42  
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);  
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)  
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-  
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)  
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)  
DE (Amyloid intracellular domain 50) (AID(50)); C31].  
GN APP OR A4 OR AD1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC TISSUE=Brain;  
 RX MEDLINE=87144572; PubMed=2881207;  
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,  
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a  
 RT cell-surface receptor.";  
 RL Nature 325:733-736(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM APP751).  
 RC TISSUE=Brain;  
 RX MEDLINE=88122639; PubMed=2893289;  
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,  
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,  
 RA Cordell B.;  
 RT "A new A4 amyloid mRNA contains a domain homologous to serine  
 RT proteinase inhibitors.";  
 RL Nature 331:525-527(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RX MEDLINE=89128427; PubMed=2783775;  
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,  
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;  
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid  
 RT is encoded by 16 exons.";  
 RL Nucleic Acids Res. 17:517-522(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM APP770).  
 RX MEDLINE=90236318; PubMed=2110105;  
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene.";  
 RL Gene 87:257-263(1990).  
 RN [5]  
 RP ERRATUM, AND REVISIONS.  
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;  
 RL Gene 102:291-292(1991).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=92268136; PubMed=1587857;  
 RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,  
 RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;  
 RT "Identification and differential expression of a novel alternative  
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in  
 RT leukocytes and brain microglial cells.";  
 RL J. Biol. Chem. 267:10804-10809(1992).  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM APP770).  
 RX MEDLINE=97263807; PubMed=9108164;  
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,  
 RA Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for  
 RT sequencing of a 300 kb region of human APP locus.";  
 RL Nucleic Acids Res. 25:1802-1808(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORM APP639).

RC TISSUE=Brain;  
 RX MEDLINE=22744650; PubMed=12859342;  
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;  
 RT "Identification of a novel alternative splicing isoform of human  
 RT amyloid precursor protein gene, APP639.";  
 RL Eur. J. Neurosci. 18:102-108(2003).  
 RN [9]  
 RP SEQUENCE FROM N.A. (ISOFORM APP305).  
 RC TISSUE=Pancreas;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [10]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89016647; PubMed=3140222;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide.";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [11]  
 RP ERRATUM, AND REVISIONS.  
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;  
 RL Nucleic Acids Res. 16:11402-11402(1988).  
 RN [12]  
 RP SEQUENCE OF 1-75 FROM N.A.  
 RX MEDLINE=89165870; PubMed=2538123;  
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;  
 RT "Characterization of the 5'-end region and the first two exons of the  
 RT beta-protein precursor gene.";  
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).  
 RN [13]  
 RP SEQUENCE OF 18-50.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=87250462; PubMed=3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts.";  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [14]



RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).  
 RC TISSUE=Brain;  
 RX MEDLINE=89346754; PubMed=2569763;  
 RA de Sauvage F., Octave J.N.;  
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly  
 RT secreted protein.";  
 RL Science 245:651-653(1989).  
 RN [15]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC TISSUE=Brain;  
 RX MEDLINE=87231971; PubMed=3035574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RN [16]  
 RP SEQUENCE OF 286-366 FROM N.A.  
 RX MEDLINE=88122640; PubMed=2893290;  
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
 RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease.";  
 RL Nature 331:528-530(1988).  
 RN [17]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE=88122641; PubMed=2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RT protease inhibitory activity.";  
 RL Nature 331:530-532(1988).  
 RN [18]  
 RP SEQUENCE OF 507-770 FROM N.A.  
 RC TISSUE=Brain cortex;  
 RX MEDLINE=88124954; PubMed=2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [19]  
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.  
 RX MEDLINE=96139497; PubMed=8576160;  
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;  
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and  
 RT mapping of the binding sites on APP and collagen type I.";  
 RL J. Biol. Chem. 271:1613-1620(1996).  
 RN [20]  
 RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717  
 RP AND AD GLY-717.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 RT mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 RN [21]  
 RP SEQUENCE OF 656-737 FROM N.A.



```

Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIVITL 720
Qy      646 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
Db      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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# RESULT 2

## A4\_MACFA

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ID      A4 MACFA          STANDARD;          PRT;      770 AA.
AC      P53601; Q95KN7;
DT      01-OCT-1996 (Rel. 34, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE      amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE      Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE      APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE      Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE      (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE      secretase C-terminal fragment 50); C31].
GN      APP.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9541;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC      TISSUE=Cerebellum;
RX      MEDLINE=91273117; PubMed=1905108;
RA      Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT      "Homology of the amyloid beta protein precursor in monkey and human
RT      supports a primate model for beta amyloidosis in Alzheimer's
RT      disease.";
RL      Am. J. Pathol. 138:1423-1435(1991).
CC      -!- FUNCTION: Functions as a cell surface receptor and performs
CC      physiological functions on the surface of neurons relevant to
CC      neurite growth, neuronal adhesion and axonogenesis. Involved in
CC      cell mobility and transcription regulation through protein-protein
CC      interactions (By similarity). Can promote transcription activation
CC      through binding to APBB1/Tip60 and inhibit Notch signaling through
CC      interaction with Numb (By similarity). Couples to apoptosis-
CC      inducing pathways such as those mediated by G(0) and JIP (By
CC      similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC      Acts as a kinesin I membrane receptor, mediating the axonal
CC      transport of beta-secretase and presenilin 1 (By similarity). May
CC      be involved in copper homeostasis/oxidative stress through copper
CC      ion reduction. In vitro, copper-metallated APP induces neuronal
CC      death directly or is potentiated through Cu(II)-mediated low-
CC      density lipoprotein oxidation (By similarity). Can regulate
CC      neurite outgrowth through binding to components of the
CC      extracellular matrix such as heparin and collagen I and IV (By
CC      similarity). The splice isoforms that contain the BPTI domain
CC      possess protease inhibitor activity (By similarity).
CC      -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

```

CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron (By similarity).  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding  
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also  
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2  
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.  
 CC In vitro, it binds MAPT via the MT-binding domains (By  
 CC similarity). Associates with microtubules in the presence of ATP  
 CC and in a kinesin-dependent manner (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the  
 CC endoplasmic reticulum) moves to the Golgi complex where complete  
 CC maturation occurs (O-glycosylated and sulfated). After alpha-  
 CC secretase cleavage, soluble APP is released into the extracellular  
 CC space and the C-terminal is internalized to endosomes and  
 CC lysosomes. Some APP accumulates in secretory transport vesicles  
 CC leaving the late Golgi compartment and returns to the cell  
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm  
 CC and nuclei of neurons (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=APP770;  
 CC IsoId=P53601-1; Sequence=Displayed;  
 CC Name=APP695;  
 CC IsoId=P53601-2; Sequence=VSP\_000010, VSP\_000011;  
 CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for  
 CC sorting of membrane proteins to the basolateral surface of  
 CC epithelial cells (By similarity).  
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-  
 CC phosphorylated proteins is required for the specific binding of  
 CC the PID domain. However additional amino acids either N- or C-  
 CC terminal to the NPXY motif are often required for complete  
 CC interaction. The PID domain-containing proteins which bind APP  
 CC require the YENPTY motif for full interaction. These interactions  
 CC are independent of phosphorylation on the terminal tyrosine  
 CC residue. The NPXY site is also involved in clathrin-mediated  
 CC endocytosis (By similarity).  
 CC -!- PTM: Proteolytically processed under normal cellular conditions.  
 CC Cleavage by alpha-secretase or alternatively by beta-secretase  
 CC leads to generation and extracellular release of soluble APP  
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the  
 CC retention of corresponding membrane-anchored C-terminal fragments,  
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase  
 CC yields P3 peptides. This is the major secretory pathway and is  
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated  
 CC gamma-secretase processing of C99 releases the amyloid beta  
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),  
 CC major components of amyloid plaques, and the cytotoxic C-terminal  
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By  
 CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis  
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9  
 CC results in the production of the neurotoxic C31 peptide and the  
 CC increased production of beta-amyloid peptides (By similarity).  
 CC -!- PTM: N- and O-glycosylated (By similarity).  
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and  
 CC serine residues is neuron-specific. Phosphorylation can affect APP  
 CC processing, neuronal differentiation and interaction with other  
 CC proteins (By similarity).  
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and  
 CC zinc, can induce histidine-bridging between beta-amyloid molecules  
 CC resulting in beta-amyloid-metal aggregates (By similarity).  
 CC Extracellular zinc-binding increases binding of heparin to APP and  
 CC inhibits collagen-binding (By similarity).  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----  
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DR EMBL; M58727; AAA36829.1; -.  
 DR EMBL; M58726; AAA36828.1; -.  
 DR HSSP; P05067; 1AAP.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;  
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;  
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;  
 KW Proteoglycan; Alternative splicing; Amyloid.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.  
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).  
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).  
 FT CHAIN 672 770 C99 (POTENTIAL).  
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).  
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).  
 FT CHAIN 688 770 C83 (POTENTIAL).  
 FT CHAIN 688 713 P3(42) (POTENTIAL).

FT	CHAIN	688	711	P3(40) (POTENTIAL).
FT	CHAIN	712	770	GAMMA-CTF(59) (POTENTIAL).
FT	CHAIN	714	770	GAMMA-CTF(57) (POTENTIAL).
FT	CHAIN	721	770	GAMMA-CTF(50) (POTENTIAL).
FT	CHAIN	740	770	C31 (POTENTIAL).
FT	DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	700	723	POTENTIAL.
FT	DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	291	341	BPTI/KUNITZ INHIBITOR.
FT	DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA
FT				(BY SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION
FT				(BY SIMILARITY).
FT	ACT SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT	SITE	671	672	CLEAVAGE (BY BETA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT				(BY SIMILARITY).
FT	SITE	724	734	BASOLATERAL SORTING SIGNAL
FT				(BY SIMILARITY).
FT	SITE	739	740	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

Query Match 98.3%; Score 3590.5; DB 1; Length 770;  
 Best Local Similarity 90.1%; Pred. No. 9.8e-169;  
 Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLMHMNVQNGKWSDPSG	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLMHMNVQNGKWSDPSG	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Qy      241 EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVR----- 288
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEAETGPC 300
Qy      289 ----- 288
Db      301 RAMISRWFVDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSVMSQSLRKTTRPLTRD 360
Qy      289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
      :||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
Qy      346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
Qy      406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Qy      466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTET 525
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTET 600
Qy      526 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 585
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Qy      586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy      646 VMLKKKQYTSIHGHVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 VMLKKKQYTSIHGHVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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RESULT 3

A4\_SAISC

ID A4\_SAISC STANDARD; PRT; 751 AA.

AC Q95241;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid

DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble

DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);

DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-

DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)

DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-

DE secretase C-terminal fragment 50); C31].

GN APP.

OS Saimiri sciureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
 OX NCBI\_TaxID=9521;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney, and Liver;  
 RX MEDLINE=96108492; PubMed=8532114;  
 RA Levy E., Amorim A., Frangione B., Walker L.C.;  
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with  
 RT cerebral amyloid angiopathy.";  
 RL Neurobiol. Aging 16:805-808(1995).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions (By similarity). Can promote transcription activation  
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through  
 CC interaction with Numb (By similarity). Couples to apoptosis-  
 CC inducing pathways such as those mediated by G(0) and JIP (By  
 CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).  
 CC Acts as a kinesin I membrane receptor, mediating the axonal  
 CC transport of beta-secretase and presenilin 1 (By similarity). May  
 CC be involved in copper homeostasis/oxidative stress through copper  
 CC ion reduction. In vitro, copper-metallated APP induces neuronal  
 CC death directly or is potentiated through Cu(II)-mediated low-  
 CC density lipoprotein oxidation (By similarity). Can regulate  
 CC neurite outgrowth through binding to components of the  
 CC extracellular matrix such as heparin and collagen I and IV (By  
 CC similarity). The splice isoforms that contain the BPTI domain  
 CC possess protease inhibitor activity (By similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron (By similarity).  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding  
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also  
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2  
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.  
 CC In vitro, it binds MAPT via the MT-binding domains (By  
 CC similarity). Associates with microtubules in the presence of ATP  
 CC and in a kinesin-dependent manner (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the  
 CC endoplasmic reticulum) moves to the Golgi complex where complete  
 CC maturation occurs (O-glycosylated and sulfated). After alpha-  
 CC secretase cleavage, soluble APP is released into the extracellular  
 CC space and the C-terminal is internalized to endosomes and  
 CC lysosomes. Some APP accumulates in secretory transport vesicles  
 CC leaving the late Golgi compartment and returns to the cell  
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm  
 CC and nuclei of neurons (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;



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CC      Comment=Additional isoforms seem to exist;
CC      Name=APP770;
CC      IsoId=Q95241-1; Sequence=Displayed;
CC      Name=APP695;
CC      IsoId=Q95241-2; Sequence=Not described;
CC      -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC      sorting of membrane proteins to the basolateral surface of
CC      epithelial cells (By similarity).
CC      -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC      phosphorylated proteins is required for the specific binding of
CC      the PID domain. However additional amino acids either N- or C-
CC      terminal to the NPXY motif are often required for complete
CC      interaction. The PID domain-containing proteins which bind APP
CC      require the YENPTY motif for full interaction. These interactions
CC      are independent of phosphorylation on the terminal tyrosine
CC      residue. The NPXY site is also involved in clathrin-mediated
CC      endocytosis (By similarity).
CC      -!- PTM: Proteolytically processed under normal cellular conditions.
CC      Cleavage by alpha-secretase or alternatively by beta-secretase
CC      leads to generation and extracellular release of soluble APP
CC      peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC      retention of corresponding membrane-anchored C-terminal fragments,
CC      C83 and C99. Subsequent processing of C83 by gamma-secretase
CC      yields P3 peptides. This is the major secretory pathway and is
CC      nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC      gamma-secretase processing of C99 releases the amyloid beta
CC      proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC      major components of amyloid plaques, and the cytotoxic C-terminal
CC      fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC      similarity).
CC      -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC      (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC      results in the production of the neurotoxic C31 peptide and the
CC      increased production of beta-amyloid peptides (By similarity).
CC      -!- PTM: N- and O-glycosylated (By similarity).
CC      -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC      serine residues is neuron-specific. Phosphorylation can affect APP
CC      processing, neuronal differentiation and interaction with other
CC      proteins (By similarity).
CC      -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC      zinc, can induce histidine-bridging between beta-amyloid molecules
CC      resulting in beta-amyloid-metal aggregates (By similarity).
CC      Extracellular zinc-binding increases binding of heparin to APP and
CC      inhibits collagen-binding (By similarity).
CC      -!- SIMILARITY: Belongs to the APP family.
CC      -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; S81024; AAD14347.1; -.
DR      HSSP; P05067; 1AAP.

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DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;  
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;  
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;  
 KW Proteoglycan; Amyloid; Alternative splicing.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 751 A4 PROTEIN.  
 FT CHAIN 18 668 SOLUBLE APP-ALPHA (POTENTIAL).  
 FT CHAIN 18 652 SOLUBLE APP-BETA (POTENTIAL).  
 FT CHAIN 653 751 C99 (POTENTIAL).  
 FT CHAIN 653 694 BETA-AMYLOID PROTEIN 42 (POTENTIAL).  
 FT CHAIN 653 692 BETA-AMYLOID PROTEIN 40 (POTENTIAL).  
 FT CHAIN 669 751 C83 (POTENTIAL).  
 FT CHAIN 669 694 P3(42) (POTENTIAL).  
 FT CHAIN 669 692 P3(40) (POTENTIAL).  
 FT CHAIN 693 751 GAMMA-CTF(59) (POTENTIAL).  
 FT CHAIN 695 751 GAMMA-CTF(57) (POTENTIAL).  
 FT CHAIN 702 751 GAMMA-CTF(50) (POTENTIAL).  
 FT CHAIN 721 751 C31 (POTENTIAL).  
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 681 704 POTENTIAL.  
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).  
 FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.  
 FT DOMAIN 316 344 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 363 428 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 504 521 COLLAGEN-BINDING (BY SIMILARITY).  
 FT DOMAIN 713 732 INTERACTION WITH G(O)-ALPHA  
 FT (BY SIMILARITY).  
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 274 280 POLY-THR.  
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION  
 FT (BY SIMILARITY).  
 FT ACT\_SITE 301 302 REACTIVE BOND.  
 FT SITE 652 653 CLEAVAGE (BY BETA-SECRETASE)  
 FT (BY SIMILARITY).  
 FT SITE 653 654 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).  
 FT SITE 668 669 CLEAVAGE (BY ALPHA-SECRETASE)  
 FT (BY SIMILARITY).  
 FT SITE 685 685 INVOLVED IN FREE RADICAL PROPAGATION  
 FT (BY SIMILARITY).

FT	SITE	687	687	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	692	693	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	694	695	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	701	702	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT				(BY SIMILARITY).
FT	SITE	705	715	BASOLATERAL SORTING SIGNAL
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT				(BY SIMILARITY).
FT	SITE	738	741	ENDOCYTOSIS SIGNAL.
FT	SITE	740	743	NPXY MOTIF.

Query Match 98.2%; Score 3584; DB 1; Length 751;  
 Best Local Similarity 92.0%; Pred. No. 2e-168;  
 Matches 691; Conservative 2; Mismatches 2; Indels 56; Gaps 1;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRDRKQCKTHPHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDHVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGEDGVEVEEEAEPYEEATERTTSIATTTTTTTTESVEEVVR-----	288
Db	241	EADDDDEDGEDGVEVEEEAEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	289	-----VPTTAASTPDAVDKYL	304
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVIPTTAASTPDAVDKYL	360
Qy	305	ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKV	364
Db	361	ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKV	420
Qy	365	ESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVNMLKKYVR	424
Db	421	ESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVNMLKKYVR	480
Qy	425	AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVAEEIQ	484
Db	481	AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVAEEIQ	540
Qy	485	DEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ	544

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Db      541 DEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQ 600
QY      545 PWSHFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEI SEVKMDAEFRHDS 604
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 PWSHFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTNIKTEEI SEVKMDAEFRHDS 660
QY      605 GYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 664
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GYEVHHQKL VFFAEDVGSNKGAI IGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 720
QY      665 AAVTPEERHLSKMQONGYENPTYKFFEQMQN 695
        ||||||||||||||||||||||||||||||||||
Db      721 AAVTPEERHLSKMQONGYENPTYKFFEQMQN 751

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#### RESULT 4

##### A4\_PIG

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ID      A4_PIG          STANDARD;      PRT;      770 AA.
AC      P79307; Q29023; Q9TUI0;
DT      01-NOV-1997 (Rel. 35, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE      amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE      Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE      APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE      Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE      (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE      secretase C-terminal fragment 50); C31].
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kimura A., Takahashi T.;
RT      "Amyloid precursor protein 770.";
RL      Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE OF 1-136 FROM N.A.
RC      TISSUE=Small intestine;
RA      Winteroe A.K., Fredholm M.;
RT      "Evaluation and characterization of a porcine small intestine cDNA
RT      library.";
RL      Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE OF 667-723 FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -!- FUNCTION: Functions as a cell surface receptor and performs
CC      physiological functions on the surface of neurons relevant to
CC      neurite growth, neuronal adhesion and axonogenesis. Involved in

```

cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G(0) and JIP (By similarity). Inhibits G(0) alpha ATPase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction (By similarity). In vitro, copper-metallated APP induces neuronal death directly or is potentiated through Cu(II)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity).

-!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).

-!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

-!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FPRL1, APPBP1, IBL, KNS2 (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1. In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

-!- DOMAIN: The basolateral sorting signal (BaSS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

-!- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the

CC retention of corresponding membrane-anchored C-terminal fragments,  
CC C83 and C99. Subsequent processing of C83 by gamma-secretase  
CC yields P3 peptides. This is the major secretory pathway and is  
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated  
CC gamma-secretase processing of C99 releases the amyloid beta  
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),  
CC major components of amyloid plaques, and the cytotoxic C-terminal  
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By  
CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis  
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9  
CC results in the production of the neurotoxic C31 peptide and the  
CC increased production of beta-amyloid peptides (By similarity).

CC -!- PTM: N- and O-glycosylated (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and  
CC serine residues is neuron-specific. Phosphorylation can affect APP  
CC processing, neuronal differentiation and interaction with other  
CC proteins (By similarity).

CC -!- PTM: Extracellular binding and reduction of copper, results in a  
CC corresponding oxidation of Cys-144 and Cys-158, and the formation  
CC of a disulfide bond (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and  
CC zinc, can induce histidine-bridging between beta-amyloid molecules  
CC resulting in beta-amyloid-metal aggregates (By similarity).  
CC Extracellular zinc-binding increases binding of heparin to APP and  
CC inhibits collagen-binding (By similarity).

CC -!- SIMILARITY: Belongs to the APP family.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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CC -----

DR EMBL; AB032550; BAA84580.1; -.

DR EMBL; Z84022; CAB06313.1; -.

DR EMBL; X56127; CAA39592.1; -.

DR HSSP; P05067; 1AAP.

DR InterPro; IPR008155; A4\_APP.

DR InterPro; IPR008154; A4\_extra.

DR InterPro; IPR002223; Kunitz\_BPTI.

DR Pfam; PF02177; A4\_EXTRA; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Kunitz\_BPTI; 1.

DR SMART; SM00006; A4\_EXTRA; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4\_EXTRA; 1.

DR PROSITE; PS00320; A4\_INTRA; 1.

DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.

DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.

KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;

KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;

KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;



```

Db      61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG 120
Qy      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Qy      181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||:|||||
Db      181 GVEFVCCPLAEESDNIDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVADVVEE 240
Qy      241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVR----- 288
        ||:|||||
Db      241 EAEDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC 300
Qy      289 ----- 288
Db      301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVMSQSLLKTTQEHLPQD 360
Qy      289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345
        :|||||
Db      361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
Qy      346 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
        |||
Db      421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
Qy      406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
        |||
Db      481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Qy      466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNLMPSLTET 525
        |||
Db      541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNLMPSLTET 600
Qy      526 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTN 585
        |||
Db      601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDPARPAADRGLTTRPGSGLTN 660
Qy      586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
        |||
Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy      646 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
        |||
Db      721 VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

```

# RESULT 5

A4\_CAVPO

ID A4\_CAVPO STANDARD; PRT; 770 AA.

AC Q60495; Q60496;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease

DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);

DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid



DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);  
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-  
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].  
 GN APP.  
 OS *Cavia porcellus* (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; *Cavia*.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Brain, and Liver;  
 RX MEDLINE=97236426; PubMed=9116031;  
 RA Beck M., Mueller D., Bigl V.;  
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and  
 RT alternative splicing."  
 RL Biochim. Biophys. Acta 1351:17-21(1997).  
 RN [2]  
 RP INTERACTION OF BETA-APP40 WITH APOE.  
 RX MEDLINE=98007700; PubMed=9349544;  
 RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,  
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;  
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on  
 RT cerebral capillary sequestration and blood-brain barrier transport of  
 RT circulating Alzheimer's amyloid beta."  
 RL J. Neurochem. 69:1995-2004(1997).  
 RN [3]  
 RP PROCESSING.  
 RX MEDLINE=20084499; PubMed=10619481;  
 RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,  
 RA Bigl V.;  
 RT "Guinea-pig primary cell cultures provide a model to study expression  
 RT and amyloidogenic processing of endogenous amyloid precursor  
 RT protein."  
 RL Neuroscience 95:243-254(2000).  
 RN [4]  
 RP GAMMA-SECRETASE PROCESSING.  
 RX MEDLINE=20576391; PubMed=11035007;  
 RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,  
 RA Ziani-Cherif C., Onstead L., Sambamurti K.;  
 RT "A novel gamma -secretase assay based on detection of the putative  
 RT C-terminal fragment-gamma of amyloid beta protein precursor."  
 RL J. Biol. Chem. 276:481-487(2001).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions (By similarity). Can promote transcription activation  
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through  
 CC interaction with Numb (By similarity). Couples to apoptosis-  
 CC inducing pathways such as those mediated by G(0) and JIP (By  
 CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).  
 CC Acts as a kinesin I membrane receptor, mediating the axonal  
 CC transport of beta-secretase and presenilin 1 (By similarity). May  
 CC be involved in copper homeostasis/oxidative stress through copper  
 CC ion reduction (By similarity). In vitro, copper-metallated APP  
 CC induces neuronal death directly or is potentiated through Cu(II)-  
 CC mediated low-density lipoprotein oxidation (By similarity). Can

CC regulate neurite outgrowth through binding to components of the  
 CC extracellular matrix such as heparin and collagen I and IV (By  
 CC similarity). The splice isoforms that contain the BPTI domain  
 CC possess protease inhibitor activity (By similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins  
 CC and apolipoproteins E and J in the CSF and to HDL particles in  
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.  
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the  
 CC extracellular matrix and may regulate neurite outgrowth in the  
 CC brain (By similarity).  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also  
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2  
 CC (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).  
 CC Associates with microtubules in the presence of ATP and in a  
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds  
 CC all three isoforms of APOE, in vitro and in vivo. When lipidated,  
 CC ApoE3 appears to be the preferred amyloid binding isoform, while  
 CC the apoE4 isoform-beta-APP40 complex is capable of being  
 CC transported across the blood-brain barrier.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated pits  
 CC (By similarity). During maturation, the immature APP (N-  
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi  
 CC complex where complete maturation occurs (O-glycosylated and  
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble  
 CC APP is released into the extracellular space and the C-terminal is  
 CC internalized to endosomes and lysosomes (By similarity). Some APP  
 CC accumulates in secretory transport vesicles leaving the late Golgi  
 CC compartment and returns to the cell surface (By similarity). APP  
 CC sorts to the basolateral surface in epithelial cells (By  
 CC similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms, missing exons 7,8 and 15, seem to  
 CC exist. The L-isoforms, missing exon 15, are referred to as  
 CC appicans;  
 CC Name=APP770;  
 CC IsoId=Q60495-1; Sequence=Displayed;  
 CC Name=APP695;  
 CC IsoId=Q60495-2; Sequence=VSP\_007221, VSP\_007222;  
 CC -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in  
 CC brain. The longer isoforms containing the BPTI domain are  
 CC predominantly expressed in peripheral organs such as muscle and  
 CC liver.  
 CC -!- INDUCTION: Increased levels during neuronal differentiation.  
 CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for  
 CC sorting of membrane proteins to the basolateral surface of  
 CC epithelial cells.  
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-  
 CC phosphorylated proteins is required for the specific binding of

CC the PID domain. However additional amino acids either N- or C-  
 CC terminal to the NPXY motif are often required for complete  
 CC interaction. The PID domain-containing proteins which bind APP  
 CC require the YENPTY motif for full interaction. These interactions  
 CC are independent of phosphorylation on the terminal tyrosine  
 CC residue (By similarity). The NPXY site is also involved in  
 CC clathrin-mediated endocytosis.

CC -!- PTM: Proteolytically processed under normal cellular conditions.  
 CC Cleavage by alpha-secretase or alternatively by beta-secretase  
 CC leads to generation and extracellular release of soluble APP  
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the  
 CC retention of corresponding membrane-anchored C-terminal fragments,  
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by  
 CC gamma-secretase yields P3 peptides. This is the major secretory  
 CC pathway and is nonamyloidogenic. Alternatively,  
 CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-  
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)  
 CC and amyloid-beta 42 (Abeta42), major components of amyloid  
 CC plaques, and the corresponding cytotoxic C-terminal fragments  
 CC (CTFs).

CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal  
 CC apoptosis (By similarity).

CC -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to  
 CC the L-APP isoforms produces the APP proteoglycan core proteins,  
 CC the appicans (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and  
 CC serine residues is neuron-specific (By similarity).  
 CC Phosphorylation can affect APP processing, neuronal  
 CC differentiation and interaction with other proteins.

CC -!- PTM: Extracellular binding and reduction of copper, results in a  
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation  
 CC of a disulfide bond (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and  
 CC zinc, can induce histidine-bridging between beta-amyloid molecules  
 CC resulting in beta-amyloid-metal aggregates.

CC -!- SIMILARITY: Belongs to the APP family.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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 CC -----

DR EMBL; X97631; CAA66230.1; -.  
 DR EMBL; X99198; CAA67589.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.

DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;  
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;  
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;  
 KW Proteoglycan; Alternative splicing; Amyloid.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.  
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (BY SIMILARITY).  
 FT CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).  
 FT CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).  
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).  
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).  
 FT CHAIN 688 770 CTF-BETA (BY SIMILARITY).  
 FT CHAIN 688 713 P3(42) (BY SIMILARITY).  
 FT CHAIN 688 711 P3(40) (BY SIMILARITY).  
 FT CHAIN 712 770 GAMMA-CTF(59) (BY SIMILARITY).  
 FT CHAIN 714 770 GAMMA-CTF(57) (BY SIMILARITY).

Query Match 96.5%; Score 3522.5; DB 1; Length 770;  
 Best Local Similarity 88.2%; Pred. No. 2.1e-165;  
 Matches 679; Conservative 7; Mismatches 9; Indels 75; Gaps 1;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGK 60  
 ||| ||||| |||||||||||||||||||||||||:|||||||: |||||  
 Db 1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLNHMHMNVQNGKWEPSGK 60  
 Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120  
 ||| :||||| ||||||||||||||||||| |||||||||||||||||  
 Db 61 TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG 120  
 Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180  
 |||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180  
 Qy 181 GVEFVCCPLAEESDNVDSADAEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEE 240  
 |||||||||||||:||||| |||||||||||||||||||:|||  
 Db 181 GVEFVCCPLAEESDNIDSADAEDDSDVWVGADTDYADGSEDKVVEVAEEEEVADVEE 240  
 Qy 241 EADDDDEDGEDGVEVEEAEEPYEEATERTTSIATTTTTTTTSEVEEVV----- 288  
 ||||| |||||||||||||||||:||||| |||||  
 Db 241 EADDDDEDVEDGVEVEEAEEPYEEATEKTTTSIATTTTTTTTSEVEEVVREVCSEQAETGPC 300  
 Qy 289 ----- 288  
 Db 301 RSMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVMSQNLLKTSGEFVSQG 360  
 Qy 289 ---VPTTAASTPDAVDKYLET PGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 345  
 :||||| ||||||||||||||||||| |||||||||||||||||  
 Db 361 PVKLPTTAASTPDAVDKYLET PGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420  
 Qy 346 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 405  
 |||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

```

Qy      406 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
      |||
Db      481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy      466 MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 525
      |||
Db      541 MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600

Qy      526 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTN 585
      |||
Db      601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPV DARPAADRGLTTRPGSGLTN 660

Qy      586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
      |||
Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy      646 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
      |||
Db      721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

```

# RESULT 6

## A4\_MOUSE

```

ID      A4_MOUSE          STANDARD;          PRT;    770 AA.
AC      P12023; P97487; P97942; Q99K32;
DT      01-OCT-1989 (Rel. 12, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE      amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE      Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE      (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE      40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE      C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE      (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE      (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE      (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE      50) (AID(50)); C31].
GN      APP.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM APP695).
RC      TISSUE=Brain;
RX      MEDLINE=88106489; PubMed=3322280;
RA      Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT      "Complementary DNA for the mouse homolog of the human amyloid beta
RT      protein precursor.";
RL      Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN      [2]
RP      REVISIONS.
RA      Yamada T.;
RL      Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN      [3]

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RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=92096458; PubMed=1756177;  
 RA de Strooper B., van Leuven F., van den Berghe H.;  
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse  
 RT is closer related to its human homolog than previously reported.";  
 RL Biochim. Biophys. Acta 1129:141-143(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC STRAIN=SAMP8; TISSUE=Hippocampus;  
 RX MEDLINE=21130647; PubMed=11235921;  
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,  
 RA Alvarez J., Morley J.E.;  
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid  
 RT precursor protein of senescence accelerated mouse (SAMP8).";  
 RL Biochem. Cell Biol. 79:57-67(2001).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE=92209998; PubMed=1555768;  
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
 RA Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
 RL Gene 112:189-195(1992).  
 RN [6]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).  
 RC TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Brain, and Kidney;  
 RX MEDLINE=89149813; PubMed=2493250;  
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;  
 RT "Structure and expression of the alternatively-spliced forms of mRNA  
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
 RT precursor.";  
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).

RN [8]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC STRAIN=CD-1; TISSUE=Placenta;  
 RX MEDLINE=89345111; PubMed=2569710;  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of *Mus domesticus*.";  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [9]  
 RP SEQUENCE OF 656-737 FROM N.A.  
 RC STRAIN=129/Sv;  
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,  
 RA Loring J.F., Goate A.M.;  
 RT "Introduction of six mutations into the mouse genome using 'Hit and  
 RT Run' gene-targeting: introduction of familial Alzheimer's disease  
 RT mutations into the mouse amyloid precursor protein gene and  
 RT humanization of the A-beta fragment.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [10]  
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.  
 RX MEDLINE=93287808; PubMed=8510506;  
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;  
 RT "Regional distribution of the alternatively spliced isoforms of beta  
 RT APP RNA transcript in the brain of normal, heterozygous and  
 RT homozygous weaver mutant mice as revealed by in situ hybridization  
 RT histochemistry.";  
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).  
 RN [11]  
 RP INTERACTION WITH KNS2.  
 RX MEDLINE=21010507; PubMed=11144355;  
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;  
 RT "Axonal transport of amyloid precursor protein is mediated by direct  
 RT binding to the kinesin light chain subunit of kinesin-I.";  
 RL Neuron 28:449-459(2000).  
 RN [12]  
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;  
 RP THR-743; TYR-757; ASN-759 AND TYR-762.  
 RX MEDLINE=21408156; PubMed=11517249;  
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,  
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,  
 RA Kyriakis J.M., Nishimoto I.;  
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1  
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";  
 RL J. Neurosci. 21:6597-6607(2001).  
 RN [13]  
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.  
 RX MEDLINE=22028091; PubMed=11912189;  
 RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;  
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins  
 RT with scaffold proteins of the JNK signaling cascade.";  
 RL J. Biol. Chem. 277:20070-20078(2002).  
 RN [14]  
 RP INTERACTION OF CTF PEPTIDES WITH NUMB.  
 RX MEDLINE=22008109; PubMed=12011466;  
 RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,  
 RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;  
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid

RT precursor protein binds Numb and inhibits Notch signaling.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).  
 RN [15]  
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.  
 RX MEDLINE=21437805; PubMed=11553691;  
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;  
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by  
 RT gamma-secretase is rapidly degraded but distributes partially in a  
 RT nuclear fraction of neurones in culture.";  
 RL J. Neurochem. 78:1168-1178(2001).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions. Can promote transcription activation through binding  
 CC to APBB1/Tip60 and inhibit Notch signaling through interaction  
 CC with Numb. Couples to apoptosis-inducing pathways such as those  
 CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By  
 CC similarity). Acts as a kinesin I membrane receptor, mediating the  
 CC axonal transport of beta-secretase and presenilin 1. May be  
 CC involved in copper homeostasis/oxidative stress through copper ion  
 CC reduction. Can regulate neurite outgrowth through binding to  
 CC components of the extracellular matrix such as heparin and  
 CC collagen I and IV (By similarity). The splice isoforms that  
 CC contain the BPTI domain possess protease inhibitor activity (By  
 CC similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind  
 CC only weakly transient metals and have little reducing activity due  
 CC to substitutions of transient metal chelating residues. Beta-APP42  
 CC may activate mononuclear phagocytes in the brain and elicit  
 CC inflammatory responses. Promotes both tau aggregation and TPK II-  
 CC mediated phosphorylation (By similarity).  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis.  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits  
 CC its serine phosphorylation. Also interacts with GPCR-like protein  
 CC BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via  
 CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the  
 CC MT-binding domains (By similarity). Associates with microtubules  
 CC in the presence of ATP and in a kinesin-dependent manner (By  
 CC similarity). Interacts, through a C-terminal domain, with GNAO1  
 CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal  
 CC neurons (By similarity). Beta-amyloid associates with HADH2 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the  
 CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 95.7%; Score 3493.5; DB 1; Length 770;  
 Best Local Similarity 87.8%; Pred. No. 5.5e-164;  
 Matches 676; Conservative 6; Mismatches 13; Indels 75; Gaps 1;



Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGK	60
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Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
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Db	61	TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLPCGIDKFR	180
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Db	181	GVEFVCCPLAEESDSVDSADAEEEDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVR-----	288
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Db	241	EADDDDEDVEDGDEVEEEAEPEYEEATERTTSTATTTTTTTSVEEVVREVCSEQAETGPC	300
Qy	289	-----	288
Db	301	RAMISRWFYFDVTEGKCVFFYGGCGGNRNNFDTEEYCMVCGSVSTQSLLKTTSEPLPQD	360
Qy	289	---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	345
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Db	361	PDKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	346	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	405
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Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	406	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	465
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Db	481	QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	466	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	525
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Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET	600
Qy	526	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	585
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Db	601	KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	586	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	645
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Db	661	IKTEEISEVKMDAEFGHDSGFVHRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	646	VMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	695
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RESULT 7

A4\_RAT

ID A4\_RAT

STANDARD;

PRT;

770 AA.

AC P08592;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid  
 DE protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble  
 DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-  
 DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);  
 DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal  
 DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);  
 DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].  
 GN APP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC TISSUE=Brain;  
 RX MEDLINE=88312583; PubMed=2900758;  
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,  
 RA Seeburg P.H.;  
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern  
 RT in rat brain suggests a role in cell contact.";  
 RL EMBO J. 7:1365-1370(1988).  
 RN [2]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89183625; PubMed=2648331;  
 RA Kang J., Mueller-Hill B.;  
 RT "The sequence of the two extra exons in rat preA4.";  
 RL Nucleic Acids Res. 17:2130-2130(1989).  
 RN [3]  
 RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.  
 RX MEDLINE=21443797; PubMed=11483588;  
 RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;  
 RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein  
 RT family resembling gamma-secretase-like cleavage of Notch.";  
 RL J. Biol. Chem. 276:35235-35238(2001).  
 RN [4]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=96187032; PubMed=8624099;  
 RA Sandbrink R., Masters C.L., Beyreuther K.;  
 RT "APP gene family. Alternative splicing generates functionally related  
 RT isoforms.";  
 RL Ann. N.Y. Acad. Sci. 777:281-287(1996).  
 RN [5]  
 RP TISSUE SPECIFICITY OF APPICAN.  
 RX MEDLINE=95263526; PubMed=7744833;  
 RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,  
 RA Mytilineou C., Margolis R.U., Robakis N.K.;  
 RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in  
 RT brain and is produced by astrocytes but not by neurons in primary  
 RT neural cultures.";  
 RL J. Biol. Chem. 270:11839-11844(1995).  
 RN [6]  
 RP TISSUE SPECIFICITY OF ISOFORMS.

RX MEDLINE=97150061; PubMed=8996834;  
 RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;  
 RT "Expression of the APP gene family in brain cells, brain development  
 RT and aging.";  
 RL Gerontology 43:119-131(1997).  
 RN [7]  
 RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND  
 RP TYR-762.  
 RX MEDLINE=99127916; PubMed=9930726;  
 RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,  
 RA Suzuki T., Nairn A.C., Greengard P.;  
 RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the  
 RT Alzheimer's amyloid precursor protein.";  
 RL J. Neurochem. 72:549-556(1999).  
 RN [8]  
 RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.  
 RX MEDLINE=99162676; PubMed=10024358;  
 RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouilliot C.,  
 RA Valenza C., Prochiantz A., Allinquant B.;  
 RT "The amyloid precursor protein interacts with Go heterotrimeric  
 RT protein within a cell compartment specialized in signal  
 RT transduction.";  
 RL J. Neurosci. 19:1717-1727(1999).  
 RN [9]  
 RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.  
 RX MEDLINE=95256193; PubMed=7737970;  
 RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;  
 RT "The chondroitin sulfate attachment site of appican is formed by  
 RT splicing out exon 15 of the amyloid precursor gene.";  
 RL J. Biol. Chem. 270:10388-10391(1995).  
 RN [10]  
 RP BETA-AMYLOID METAL-BINDING.  
 RX MEDLINE=99316162; PubMed=10386999;  
 RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,  
 RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,  
 RA Bush A.I.;  
 RT "The A beta peptide of Alzheimer's disease directly produces hydrogen  
 RT peroxide through metal ion reduction.";  
 RL Biochemistry 38:7609-7616(1999).  
 RN [11]  
 RP BETA-AMYLOID ZINC BINDING.  
 RX MEDLINE=99343552; PubMed=10413512;  
 RA Liu S.T., Howlett G., Barrow C.J.;  
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation  
 RT of the A beta peptide of Alzheimer's disease.";  
 RL Biochemistry 38:9373-9378(1999).  
 RN [12]  
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF  
 RP GLY-704.  
 RX MEDLINE=21956095; PubMed=11959460;  
 RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;  
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-  
 RT peptide 1-42-associated oxidative stress and neurotoxicity.";  
 RL Biochim. Biophys. Acta 1586:190-198(2001).  
 RN [13]  
 RP PHOSPHORYLATION.  
 RX MEDLINE=97239592; PubMed=9085254;

RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,  
 RA Greengard P., Suzuki T.;  
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is  
 RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and  
 RT cultured cells.";  
 RL Mol. Med. 3:111-123(1997).  
 RN [14]  
 RP PHOSPHORYLATION ON SER-730.  
 RX MEDLINE=99262094; PubMed=10329382;  
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,  
 RA Greengard P., Nairn A.C., Suzuki T.;  
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid  
 RT precursor protein at Ser655 by a novel protein kinase.";  
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).  
 RN [15]  
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF  
 RP THR-743.  
 RX MEDLINE=99274744; PubMed=10341243;  
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,  
 RA Kirino Y., Greengard P., Suzuki T.;  
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein  
 RT during neuronal differentiation.";  
 RL J. Neurosci. 19:4421-4427(1999).  
 RN [16]  
 RP PHOSPHORYLATION ON THR-743.  
 RX MEDLINE=20396183; PubMed=10936190;  
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,  
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;  
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor  
 RT protein by cyclin-dependent kinase 5.";  
 RL J. Neurochem. 75:1085-1091(2000).  
 RN [17]  
 RP CARBOHYDRATE STRUCTURE OF APPICAN.  
 RX MEDLINE=21463085; PubMed=11479316;  
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,  
 RA Sugahara K., Robakis N.K.;  
 RT "Appican, the proteoglycan form of the amyloid precursor protein,  
 RT contains chondroitin sulfate E in the repeating disaccharide region  
 RT and 4-O-sulfated galactose in the linkage region.";  
 RL J. Biol. Chem. 276:37155-37160(2001).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions (By similarity). Can promote transcription activation  
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through  
 CC interaction with Numb (By similarity). Couples to apoptosis-  
 CC inducing pathways such as those mediated by G(0) and JIP. Inhibits  
 CC G(0) alpha ATPase activity. Acts as a kinesin I membrane receptor,  
 CC mediating the axonal transport of beta-secretase and presenilin 1  
 CC (By similarity). May be involved in copper homeostasis/oxidative  
 CC stress through copper ion reduction. Can regulate neurite  
 CC outgrowth through binding to components of the extracellular  
 CC matrix such as heparin and collagen I and IV (By similarity). The  
 CC splice isoforms that contain the BPTI domain possess protease  
 CC inhibitor activity (By similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind  
 CC only weakly transient metals and have little reducing activity due  
 CC to substitutions of transient metal chelating residues. Beta-APP42  
 CC may activate mononuclear phagocytes in the brain and elicit  
 CC inflammatory responses. Promotes both tau aggregation and TPK II-  
 CC mediated phosphorylation (By similarity).  
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the  
 CC extracellular matrix and may regulate neurite outgrowth in the  
 CC brain.  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding  
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also  
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2  
 CC (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.  
 CC In vitro, it binds MAPT via the MT-binding domains (By  
 CC similarity). Associates with microtubules in the presence of ATP  
 CC and in a kinesin-dependent manner (By similarity). Interacts,  
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds  
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid  
 CC associates with HADH2 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 95.7%; Score 3493.5; DB 1; Length 770;  
 Best Local Similarity 87.7%; Pred. No. 5.5e-164;  
 Matches 675; Conservative 8; Mismatches 12; Indels 75; Gaps 1;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPGSGTK 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPGSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 GVEFVCCPLAEESDSIDSADAEEDDSDVWWGGADTDYADGGEDKVVEVAEEEEVADVEEEE 240

Qy    241 EADDDDEDGEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTSESVEEVVR----- 288
      ||: |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 EAEDDEDVEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTSESVEEVVREVCSEQAETGPC 300

Qy    289 ----- 288
Db    301 RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVSSQSLLKTTSEPLPQD 360

```

Qy 289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 345  
:|||||  
Db 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420  
Qy 346 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 405  
|||||  
Db 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480  
Qy 406 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465  
|||||  
Db 481 QAVPPRPHHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540  
Qy 466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 525  
|||||  
Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600  
Qy 526 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 585  
|||||  
Db 601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660  
Qy 586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645  
|||||  
Db 661 IKTEEISEVKMDAEFGHDSGYEVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720  
Qy 646 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695  
|||||  
Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

# RESULT 8

## A4\_TETFL

ID A4\_TETFL STANDARD; PRT; 780 AA.  
AC O73683;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:  
DE Beta-amyloid protein (Beta-APP) (A-beta)].  
GN APP.  
OS Tetraodon fluviatilis (Puffer fish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetradontoidea; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=47145;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98252138; PubMed=9599080;  
RA Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;  
RT "Analysis of pufferfish homologues of the AT-rich human APP gene";  
RL Gene 210:17-24(1998).  
CC -!- FUNCTION: Functional neuronal receptor which couples to  
CC intracellular signaling pathway through the GTP-binding protein  
CC G(O) (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the APP family.  
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.



Db 128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRAMNLHDYGMLLPCGIDRFRGVFEFVC 187

Qy 187 CPLAEESDNVDSADAEEDSDVWVGADTDYADGS-----EDKVVEVAEEE 232  
 || || :||| : : ||||| ||||| ||:| | ||| ||

Db 188 CP-AEAERDMDSTEKDADSDVWVGADNDYSDNSMVRPEPEAEQQEETRPSVVEEEEEEG 246

Qy 233 EVAEVEEEE-----ADDEDDEDGDEVEEEAEPEYEEATERTTSIA 273  
 |||: :||| |||:|:| ||:| | :| | ||:|

Db 247 EVAQEDDEEEEEEVLDTDQDGDGEEDHEAADDEEEEDVDEIDAFGESDDVDADAPTNNVA 306

Qy 274 ---TTTTTTTESVEEVVR----- 288  
 ||||| |||||

Db 307 MTTTTTTTTTESVEEVVRMFCWAHADTGPCTASMPSWYFDAVDGRTMYELMYGGCGGNMN 366

Qy 289 -----VPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHRERMSQ 333  
 ||| |:|||| |||| | ||||| ||||| ||||| |||||

Db 367 NFESEYCLSVCSVVPTDMPSSPDAVDHYLETPADENEHAHFQAKESLEAKHRERMSQ 426

Qy 334 VMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDR 393  
 ||||| :||| || | ||||:||||:||||| ||||| :|||

Db 427 VMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEALLNDR 486

Qy 394 RRLALENYITALQAVPPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRS 453  
 ||||| :||| ||||| :||| ||||| ||||| ||||| ||||| |||||

Db 487 RRLALENYLTALQQDPPRPRHVFSLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRP 546

Qy 454 QVMTHLRVIYERMNQSLSLYNVPAVAEEIQDEVDELLOKEQNYSDDLANMISEPRISY 513  
 ||:|||| | |||| | || | ||:|:| |||:| | |||: |||: |||: |||

Db 547 QVLTHLRVIEERMNQSLGLLYKVPGVADDIQDQV-ELLQREQAEMAQQLANLQTDVRVSY 605

Qy 514 GNDALMPSLTETKTTVELLPVNGEFSLDDLQPDWH--SFGADSVPAANTENEVEPVDARPA 571  
 ||||| :||| | :| : | || | |||:||||:|

Db 606 GNDALMPDQELGDGQADLLP--QEDTLGGVGFVHPESFN---QLNTENQVEPVDSPRPTF 659

Qy 572 DRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLFFAEDVGSNKGAIIGLM 631  
 :||: ||| :| | : |:|:| | | : ||||| ||||| ||||| ||||| |||||

Db 660 ERGVPTRP---VTGKSMEAVPELRMETEDRQSTEYEVHHQKLFFAEDVGSNKGAIIGLM 716

Qy 632 VGGVVIATVIVITLVMLKKKQYTSIIHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 691  
 ||||| :||| ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||

Db 717 VGGVVIATVIVITLVMLRKKQYTSIIHGIIEVDAAVTPEERHLSKMQQNGYENPTYKFFE 776

Qy 692 QMQN 695  
 ||||

Db 777 QMQN 780

RESULT 9

A4\_FUGRU

ID A4\_FUGRU STANDARD; PRT; 737 AA.

AC 093279;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:

DE Beta-amyloid protein (Beta-APP) (A-beta)].

GN APP.



```

OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; AF090120; AAD13392.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL          1      18      POTENTIAL.
FT   CHAIN           19     737     ALZHEIMER'S DISEASE AMYLOID A4
FT                                     PROTEIN HOMOLOG.
FT   CHAIN           639     681     BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN          19     668     EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM        669     689     POTENTIAL.
FT   DOMAIN          690     737     CYTOPLASMIC (POTENTIAL).
FT   DOMAIN          286     344     BPTI/KUNITZ INHIBITOR.
FT   SITE            726     729     CLATHRIN-BINDING (BY SIMILARITY).
FT   ACT_SITE        300     301     REACTIVE BOND.

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FT DISULFID 290 340 BY SIMILARITY.  
 FT DISULFID 299 323 BY SIMILARITY.  
 FT DISULFID 315 336 BY SIMILARITY.  
 FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 737 AA; 82856 MW; 6FAD01E2E3B2B7E2 CRC64;

Query Match 67.1%; Score 2448.5; DB 1; Length 737;  
 Best Local Similarity 64.0%; Pred. No. 6.9e-113;  
 Matches 482; Conservative 84; Mismatches 100; Indels 87; Gaps 12;

QY 7 LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGKTCTIDTK 66  
 :||| | |: |:| | ||| |||:||||:||||:||||:||||:|:|:|  
 Db 8 VLLLVATLTRSSEIPADDTVGLLTPQVAMFCGKLNMHINVQNGKWDSDPSGKTCLNTK 67

QY 67 EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA 126  
 |||||:||||:||||:||||:| | |:|||||  
 Db 68 EGILQYCQEVYPELQITNVVEANQPVSIQNWCKKGRKQCRSHTHIVPYRCLVGEFVSDA 127

QY 127 LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC 186  
 |||||: ||:|||||:| ::| |||||:||||:|  
 Db 128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVKFCV 187

QY 187 CPLAEESDNVDSADAEEEDSDVWWGGADTDYADGS---EDKVVEVAEEEEVAEVEEEAD 243  
 || || ||:: | ::||| ||| ::: | : || : | :| |  
 Db 188 CP-AETEQETDSSEVEGEESDVWWGGADPEYSENSPPTPSRATYVAGD---AFERDENG 243

QY 244 DDEDEDGDEVEEEAEPYEEATERTTSIA--TTTTTTESVEEVVR----- 288  
 |||:| | ::| | :|: ||| ::| |||||  
 Db 244 GDEDEDEDVDPTDE---QESDERTANVAMTTTTTTTTESVEEVVRVAVCWAQAESGPCR 300

QY 289 -----VPTTAASTPDAVDKYLE 305  
 :|| | | ||||:| |  
 Db 301 AMLERWYFNPKKRRCVPFLFGGCGGNRNNFESEYCLAVCSSSLPTVAPSPPPDAVDQYFE 360

QY 306 TPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQHFQEKVE 365  
 |||:|||| |:|||| |||||:|||||  
 Db 361 APGDDNEHADFRKAKESLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQHFQEKVE 420

QY 366 SLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMLKKYVRA 425  
 :||||| |||||:| | ||| |||: ||| ||| | | ::|||  
 Db 421 ALEQEAAGERQQLVETHMARVEALLNSRRRLTLENYLGALQANPPRARQVLSLLKKYVRA 480

QY 426 EQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPAVAEEIQD 485  
 |||||:|||| ||||| ||:|||| |||||:| | |||  
 Db 481 EQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIDERMNQSLALLYKVPSVASEIQN 540

QY 486 EVDELLQKEQNYSDVLANMIS---EPRI SYGNDALMPSLTETKTTVELLPVNGEFLDD 542  
 :: : | : : : : :||| | : : : | :|  
 Db 541 QIYPAAGSD---CKDPVEHCVCPOVDGLVSYGNDALMPDQAYSSAPMD-MGVDGLGSID- 595

QY 543 LQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRH 602  
 || |||| ||||| |||| ||| ::::| ||: ||: : : |  
 Db 596 ----QSFN----QANTENHVEPVDARPIPDRLPTRP---VSSLKLEEMPEVRTETDKRQ 644

QY 603 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVE 662  
 :||||:|||||:|||||:|||||:|||||:|||||:|  
 Db 645 SAGYEVYHQKLVFFADDVGSNKGAIIGLMVGGVVIATVIVITLVMLRKKQYTSIHGVIE 704

QY 663 VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695  
 |||||:|||||  
 Db 705 VDAAVTPEERHLARMQQNGYENPTYKFFEQMQN 737

RESULT 10

APP2\_MOUSE

ID APP2\_MOUSE STANDARD; PRT; 695 AA.  
 AC Q06335;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).  
 GN APLP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal brain;  
 RA von der Kammer H.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE OF 1-246 FROM N.A.  
 RX MEDLINE=94032480; PubMed=8218408;  
 RA Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;  
 RT "The complete cDNA coding sequence for the mouse CDEI binding  
 RT protein.";  
 RL Biochim. Biophys. Acta 1216:154-156(1993).  
 RN [3]  
 RP SEQUENCE OF 185-695 FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Heart;  
 RX MEDLINE=93129193; PubMed=1482349;  
 RA Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;  
 RT "A murine sequence-specific DNA binding protein shows extensive local  
 RT similarities to the amyloid precursor protein.";  
 RL Biochem. Biophys. Res. Commun. 189:1336-1341(1992).  
 RN [4]  
 RP SEQUENCE OF 1-35 FROM N.A.  
 RC STRAIN=129/Sv;  
 RX MEDLINE=96029629; PubMed=7592716;  
 RA von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,  
 RA Gilbert D.J., Jenkins N.A., Sisodia S.S.;  
 RT "The mouse APLP2 gene. Chromosomal localization and promoter  
 RT characterization.";  
 RL J. Biol. Chem. 270:25475-25480(1995).  
 CC -!- FUNCTION: Binds to the DNA 5'-GTCACATG-3' (CDEI box) which plays  
 CC an important role in the early development of embryos.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear  
 CC (Potential).  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -----  
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	Sequence	Position
Db	302 IVHDKVPPTPLPTND-VDVYLETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAE	360
Qy	343 RQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYI	402
Db	361 LQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRRRIALENYL	420
Qy	403 TALQAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI	462
Db	421 AALQSDPPRPHRILQALRRYVRAENKDRLLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVI	480
Qy	463 YERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSL	522
Db	481 EERRNQSLTLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTSSI	523
Qy	523 TETKTTVELLPVNGEFSDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSG	582
Db	524 SENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE-----GSGMAEQDG-G	566
Qy	583 LTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----NK	624
Db	567 LIGAEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEEPESVGPLREDFSLSS	624
Qy	625 GAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGHVVEVDAAVTPEERHLSKMQONGYEN	684
Db	625 NALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHYEN	684
Qy	685 PTYKFFEQMQ 694	
Db	685 PTYKYLEQMQ 694	

RC TISSUE=Ovary;  
 RX MEDLINE=95217334; PubMed=7702756;  
 RA von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;  
 RT "A human amyloid precursor-like protein is highly homologous to a  
 RT mouse sequence-specific DNA-binding protein.";  
 RL DNA Cell Biol. 13:1137-1143(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94035131; PubMed=8220435;  
 RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,  
 RA Hyman B.T., Neve R.L., Tanzi R.E.;  
 RT "Isolation and characterization of APLP2 encoding a homologue of the  
 RT Alzheimer's associated amyloid beta protein precursor.";  
 RL Nat. Genet. 5:95-99(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: May play a role in the regulation of hemostasis. The  
 CC soluble form may have inhibitory properties towards coagulation  
 CC factors. May interact with cellular G-protein signaling pathways.  
 CC May bind to the DNA 5'-GTCACATG-3'(CDEI box).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear  
 CC (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1;  
 CC IsoId=Q06481-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q06481-2; Sequence=VSP\_000018;  
 CC Name=3;  
 CC IsoId=Q06481-3; Sequence=VSP\_000019;  
 CC -!- TISSUE SPECIFICITY: In placenta, brain, heart, lung, liver, kidney  
 CC and endothelial tissues.  
 CC -!- SIMILARITY: Belongs to the APP family.

```

CC      -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; S60099; AAC60589.1; -.
DR      EMBL; L09209; AAA35526.1; -.
DR      EMBL; Z22572; CAA80295.1; -.
DR      EMBL; L27631; AAC41701.1; -.
DR      EMBL; BC000373; AAH00373.1; -.
DR      PIR; A49321; A49321.
DR      HSSP; P05067; 1MWP.
DR      Genew; HGNC:598; APLP2.
DR      MIM; 104776; -.
DR      GO; GO:0016021; C:integral to membrane; NAS.
DR      GO; GO:0005634; C:nucleus; IDA.
DR      GO; GO:0003677; F:DNA binding; NAS.
DR      GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF00014; Kunitz_BPTI; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      PRINTS; PR00759; BASICPTASE.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      SMART; SM00131; KU; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW      Transmembrane; Signal; Alternative splicing; DNA-binding;
KW      Nuclear protein; Serine protease inhibitor.
FT      SIGNAL      1      29      POTENTIAL.
FT      CHAIN       30     763     AMYLOID-LIKE PROTEIN 2.
FT      DOMAIN      30     692     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM    693     716     POTENTIAL.
FT      DOMAIN      717     763     CYTOPLASMIC (POTENTIAL).
FT      DOMAIN      215     280     ASP/GLU-RICH (HIGHLY ACIDIC).
FT      DOMAIN      306     364     BPTI/KUNITZ INHIBITOR.
FT      DOMAIN      215     231     POLY-GLU.
FT      ACT_SITE    320     321     REACTIVE BOND (BY SIMILARITY).
FT      DISULFID    310     360     BY SIMILARITY.
FT      DISULFID    319     343     BY SIMILARITY.
FT      DISULFID    335     356     BY SIMILARITY.
FT      VARSPLIC    308     363     Missing (in isoform 2).
FT                                     /FTId=VSP_000018.
FT      VARSPLIC    613     624     Missing (in isoform 3).
FT                                     /FTId=VSP_000019.
FT      CONFLICT    543     543     S -> I (IN REF. 1).
SQ      SEQUENCE    763 AA;  86955 MW;  CA3A7D6DDB8A28D0 CRC64;

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Query Match 47.3%; Score 1728; DB 1; Length 763;  
Best Local Similarity 47.1%; Pred. No. 1.3e-77;  
Matches 372; Conservative 112; Mismatches 165; Indels 140; Gaps 20;

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Qy      5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
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Db      15 LLLLLLVGLTAPALALAGYIEALAAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74

Qy      57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
      :|||:| :||| :|||||:|||||||:|||| | |:| |||:| :|||:| || |::
Db      75 TGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCRRDKKQCKS--RFVTPFK 132

Qy     117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
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Db     133 CLVGEFVSDVLLVPEKCQFFHKERMEVCENHQHWHVTVVKEACLTQGMTLYSYGMLLPCGV 192

Qy     177 DKFRGVFEVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAE 236
      |:| | |:||| : :| : |||: : : | || | :| | :
Db     193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-----EEEEDEEEDYDVYKSEFPTEAD 245

Qy     237 VEE--EEA--DDDEDEDGDEVEEEAEPEY-----EEATERTTSIATTTTTTTES 282
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Db     246 LEDFTEAAVDEDEDEEEEGEEVVEDRDYYYDTFKGDDYNEENPTEPGSDGTMSDKEITHD 305

Qy     283 VEEV-----VRVP 290
      |:| :|
Db     306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCKAMIP 365

Qy     291 TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPK 350
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Db     366 PTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPK 424

Qy     351 ADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITALQAVPP 410
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Qy     411 RPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSL 470
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Db     485 RPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLVIEERRNQSL 544

Qy     471 SLLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGN DALMPSLTETKTVE 530
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Db     545 SLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQFTASISETPVDVR 587

Qy     531 LLPVNGEFLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN----- 585
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Db     588 ---VSSEES-EEIPPFHPF--HPFPALPENE----DTQPELYHPM--KKGSGVGEQDGG 635

Qy     586 IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-----NKG 625
      | || | : |:| | :| :::| | | :
Db     636 IGAEKVINSKNKVDENMVIDETLDV--KEMIFNAERVGGLEERESVGPLREDFSLSSS 693

Qy     626 AIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENP 685
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Qy            686 TYKFFEQMQ 694  
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 Db            754 TYKYLEQMQ 762

RESULT 12

APP2\_RAT

ID    APP2\_RAT                    STANDARD;            PRT;    765 AA.  
 AC    P15943;  
 DT    01-APR-1990 (Rel. 14, Created)  
 DT    01-OCT-1996 (Rel. 34, Last sequence update)  
 DT    28-FEB-2003 (Rel. 41, Last annotation update)  
 DE    Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).  
 GN    APLP2.  
 OS    Rattus norvegicus (Rat).  
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX    NCBI\_TaxID=10116;  
 RN    [1]  
 RP    SEQUENCE OF 1-627 FROM N.A.  
 RC    STRAIN=Wistar; TISSUE=Brain, and Heart;  
 RX    MEDLINE=94368849; PubMed=8086458;  
 RA    Sandbrink R., Masters C.L., Beyreuther K.;  
 RT    "Complete nucleotide and deduced amino acid sequence of rat amyloid  
 RT    protein precursor-like protein 2 (APLP2/APPH): two amino acids length  
 RT    difference to human and murine homologues.";  
 RL    Biochim. Biophys. Acta 1219:167-170(1994).  
 RN    [2]  
 RP    SEQUENCE OF 575-765 FROM N.A.  
 RC    TISSUE=Testis;  
 RX    MEDLINE=90207205; PubMed=1690887;  
 RA    Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;  
 RT    "Characterization of cDNA encoding a human sperm membrane protein  
 RT    related to A4 amyloid protein.";  
 RL    Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).  
 CC    -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC    -!- ALTERNATIVE PRODUCTS:  
 CC        Event=Alternative splicing; Named isoforms=4;  
 CC        Name=A;  
 CC        IsoId=P15943-1; Sequence=Displayed;  
 CC        Name=B;  
 CC        IsoId=P15943-2; Sequence=VSP\_000021;  
 CC        Name=C;  
 CC        IsoId=P15943-3; Sequence=VSP\_000020;  
 CC        Name=D;  
 CC        IsoId=P15943-4; Sequence=VSP\_000020, VSP\_000021;  
 CC    -!- SIMILARITY: Belongs to the APP family.  
 CC    -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 CC    -----  
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 CC    -----

DR EMBL; X77934; CAA54906.1; -.  
 DR EMBL; M31322; AAA42352.1; -.  
 DR PIR; A35981; A35981.  
 DR PIR; S42880; S42880.  
 DR HSSP; P05067; 1MWP.  
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 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Transmembrane; Alternative splicing; Serine protease inhibitor;  
 KW Signal; Glycoprotein.  
 FT SIGNAL 1 29 POTENTIAL.  
 FT CHAIN 30 765 AMYLOID-LIKE PROTEIN 2.  
 FT DOMAIN 30 695 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 696 718 POTENTIAL.  
 FT DOMAIN 719 765 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 218 282 ASP/GLU-RICH (HIGHLY ACIDIC).  
 FT DOMAIN 308 366 BPTI/KUNITZ INHIBITOR.  
 FT ACT\_SITE 322 323 REACTIVE BOND (BY SIMILARITY).  
 FT DISULFID 312 362 BY SIMILARITY.  
 FT DISULFID 321 345 BY SIMILARITY.  
 FT DISULFID 337 358 BY SIMILARITY.  
 FT DOMAIN 218 229 POLY-GLU.  
 FT CARBOHYD 628 628 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).  
 FT VARSPLIC 311 365 Missing (in isoform C and isoform D).  
 FT /FTId=VSP\_000020.  
 FT VARSPLIC 616 627 Missing (in isoform B and isoform D).  
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 FT CONFLICT 575 577 DQF -> EFV (IN REF. 2).  
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Query Match 47.0%; Score 1716; DB 1; Length 765;  
 Best Local Similarity 46.2%; Pred. No. 4.9e-77;  
 Matches 364; Conservative 122; Mismatches 166; Indels 136; Gaps 20;

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 Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176  
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 Db 133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192



OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98088960; PubMed=9428684;  
 RA Paliga K., Peraus G., Kreger S., Duwrrwang U., Hesse L., Multhaup G.,  
 RA Masters C.L., Beyreuther K., Weidemann A.;  
 RT "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic  
 RT expression in COS-7 cells and identification of soluble forms in the  
 RT cerebrospinal fluid.";  
 RL Eur. J. Biochem. 250:354-363(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98180887; PubMed=9521588;  
 RA Lenkkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,  
 RA Olsen A., Tryggvason K.;  
 RT "Structure of the human amyloid-precursor-like protein gene APLP1 at  
 RT 19q13.1.";  
 RL Hum. Genet. 102:192-196(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.  
 RX MEDLINE=96115107; PubMed=7494461;  
 RA Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,  
 RA Black I.B.;  
 RT "Selective localization of amyloid precursor-like protein 1 in the  
 RT cerebral cortex postsynaptic density.";  
 RL Brain Res. Mol. Brain Res. 32:36-44(1995).  
 RN [5]  
 RP HEPARIN AND ZINC BINDING.  
 RX MEDLINE=95014513; PubMed=7929392;  
 RA Bush A.I., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;  
 RT "The amyloid beta-protein precursor and its mammalian homologues.  
 RT Evidence for a zinc-modulated heparin-binding superfamily.";  
 RL J. Biol. Chem. 269:26618-26621(1994).

RN [6]  
 RP INTERACTION WITH APBA2.  
 RX MEDLINE=99107877; PubMed=9890987;  
 RA Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,  
 RA Sakiyama S., Kirino Y., Suzuki T.;  
 RT "Interaction of a neuron-specific protein containing PDZ domains with  
 RT Alzheimer's amyloid precursor protein.";  
 RL J. Biol. Chem. 274:2243-2254(1999).  
 RN [7]  
 RP EXTRACELLULAR COPPER-BINDING.  
 RX MEDLINE=22130992; PubMed=12135352;  
 RA Simons A., Ruppert T., Schmidt C., Schlicksupp A., Pipkorn R.,  
 RA Reed J., Masters C.L., White A.R., Cappai R., Beyreuther K.,  
 RA Bayer T.A., Multhaup G.;  
 RT "Evidence for a copper-binding superfamily of the amyloid precursor  
 RT protein.";  
 RL Biochemistry 41:9310-9320(2000).  
 CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal  
 CC gamma-secretase processed fragment, ALID1, activates transcription  
 CC activation through APBB1 (Fe65) binding (By similarity). Couples  
 CC to JIP signal transduction through C-terminal binding. May  
 CC interact with cellular G-protein signaling pathways. Can regulate  
 CC neurite outgrowth through binding to components of the  
 CC extracellular matrix such as heparin and collagen I.  
 CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of  
 CC neuronal apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB and APBA family members,  
 CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its  
 CC serine phosphorylation (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally  
 CC processed in the Golgi complex.  
 CC -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is  
 CC localized to the postsynaptic density (PSD).  
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-  
 CC phosphorylated proteins is required for the specific binding of  
 CC the PID domain. However additional amino acids either N- or C-  
 CC terminal to the NPXY motif are often required for complete  
 CC interaction. The NPXY site is also involved in clathrin-mediated  
 CC endocytosis.  
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal  
 CC apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By  
 CC similarity).  
 CC -!- PTM: N- and O-glycosylated.  
 CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.  
 CC Zinc-binding increases heparin binding. No Cu(II) reducing  
 CC activity with copper-binding.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -----  
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 CC -----





RC TISSUE=Brain;  
 RX MEDLINE=93066322; PubMed=1279693;  
 RA Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,  
 RA Solomon F.;  
 RT "Identification of a mouse brain cDNA that encodes a protein related  
 RT to the Alzheimer disease-associated amyloid beta protein precursor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
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 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
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 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP COLLAGEN-BINDING.  
 RX MEDLINE=96139497; PubMed=8576160;  
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;  
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and  
 RT mapping of the binding sites on APP and collagen type I.";  
 RL J. Biol. Chem. 271:1613-1620(1996).  
 RN [4]  
 RP INTERACTION WITH DAB1.  
 RX MEDLINE=99389880; PubMed=10460257;  
 RA Homayouni R., Rice D.S., Sheldon M., Curran T.;  
 RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like  
 RT protein 1.";  
 RL J. Neurosci. 19:7507-7515(1999).  
 RN [5]  
 RP INTERACTION WITH MAPK8IP1.  
 RX MEDLINE=21408156; PubMed=11517249;  
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,  
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,  
 RA Kyriakis J.M., Nishimoto I.;  
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1  
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";  
 RL J. Neurosci. 21:6597-6607(2001).  
 RN [6]  
 RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF  
 RP TYR-641.



RX MEDLINE=22313598; PubMed=12228233;  
 RA Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;  
 RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-  
 RT secretase regulates transcription."  
 RL J. Biol. Chem. 277:44195-44201(2002).  
 CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal  
 CC gamma-secretase processed fragment, ALID1, activates transcription  
 CC activation through APBB1 (Fe65) binding. Couples to JIP signal  
 CC transduction through C-terminal binding. May interact with  
 CC cellular G-protein signaling pathways. Can regulate neurite  
 CC outgrowth through binding to components of the extracellular  
 CC matrix such as heparin and collagen I.  
 CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of  
 CC neuronal apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB and APBA family members,  
 CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its  
 CC serine phosphorylation.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally  
 CC processed in the Golgi complex.  
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-  
 CC phosphorylated proteins is required for the specific binding of  
 CC the PID domain. However additional amino acids either N- or C-  
 CC terminal to the NPXY motif are often required for complete  
 CC interaction. The NPXY site is also involved in clathrin-mediated  
 CC endocytosis.  
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal  
 CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By  
 CC similarity).  
 CC -!- PTM: N- and O-glycosylated.  
 CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.  
 CC Zinc-binding increases heparin binding. No Cu(II) reducing  
 CC activity with copper-binding.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -----  
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 CC -----  
 DR EMBL; L04538; AAA37247.1; -.  
 DR EMBL; BC021877; AAH21877.1; -.  
 DR PIR; A46362; A46362.  
 DR HSSP; P05067; 1MWP.  
 DR MGD; MGI:88046; Aplp1.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;  
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;

KW Glycoprotein.

FT	SIGNAL	1	37	POTENTIAL.
FT	CHAIN	38	653	AMYLOID-LIKE PROTEIN 1.
FT	CHAIN	624	653	C30 (BY SIMILARITY).
FT	DOMAIN	38	583	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	584	606	POTENTIAL.
FT	DOMAIN	607	653	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	157	177	COPPER-BINDING.
FT	DOMAIN	203	210	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	313	345	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	413	444	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	445	462	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	263	271	POLY-GLU.
FT	DOMAIN	535	538	POLY-SER.
FT	DOMAIN	601	606	POLY-LEU.
FT	SITE	166	166	REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT	SITE	607	618	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FT	SITE	623	624	CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT	SITE	641	644	ENDOCYTOSIS SIGNAL.
FT	SITE	643	646	NPXY MOTIF.
FT	CARBOHYD	464	464	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	554	554	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MUTAGEN	641	641	Y->G: REDUCED BINDING OF APBB1.
FT	CONFLICT	17	17	P -> PP (IN REF. 2).
SQ	SEQUENCE	653 AA; 72750 MW; 56516DC3EA40E4B0 CRC64;		

Query Match 32.5%; Score 1185; DB 1; Length 653;  
 Best Local Similarity 38.6%; Pred. No. 3.9e-51;  
 Matches 270; Conservative 121; Mismatches 231; Indels 78; Gaps 17;

Qy	1	MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRNLNMHNVQNGKWDSDPSGT	59
Db	22	LLP-LSLLLLRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGRLLTLHRDLRTGRWEPDPQRS	80
Qy	60	KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL	118
Db	81	RRCLLDPPQRVLEYCRQMPYELHIARVEQAAQAI PMERWCGGTRSGRCAHPHHEVVPFHCL	140
Qy	119	VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK	178
Db	141	PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGS GMLLPCGSDR	200
Qy	179	FRGVEFVCCPLAEE SDNVD SADA EEDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV	237
Db	201	FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-----EEEVESF	248
Qy	238	EEEEADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTTESVEEVVRVPTTAASP	297
Db	249	PQPVDDYFVEPPQAE EEEEEEEERAPPPSSHTPVMVSRVTPTPR-----PT-----	294
Qy	298	DAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVI	357
Db	295	DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMADSQSKNLPKADRQALN	354
Qy	358	QHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFN	417

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      :|||  ::||:: : |||:||||  || |::||:| ||| :: |||  ||:  |
Db      355 EHFQSILQTL EEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQAERVLM 414

QY      418 MLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP 477
      |::|:|||||:::||||:|::||  |||:| | :| || |||:| | ||||| | |  |
Db      415 ALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRQVQTHLQVIEERMNQSLGLLDQNP 474

QY      478 AVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMP-SLTETKTTVELLPVNG 536
      :|:|:: :: |||  || :  :  || :| | :| |
Db      475 HLAQELRPQIQELL-----LAEHLGPSEL----DASVPGSSSEDK----- 510

QY      537 EFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 596
      |||  |:: :|  | :| | : |  | : : :
Db      511 ----GSLQP-----PESKDDPPVTLP---KGSTDQESSSSGREKLTPLEQYEQ 551

QY      597 DAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML-KKKQ 652
      |: |  |:  | :: |: ||: |  ::||::|::| |||
Db      552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSRREALSGLLIMGAGGSLIVLSLLLLRKKKP 611

QY      653 YTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 692
      | :| ||||| | :| ||: | ::|::| |||||:| | :
Db      612 YGTISHGVVEVDPMLTLEEQQQLRELQRHGYENPTYRFLEE 651

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# RESULT 15

## A4\_CAEEL

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ID      A4_CAEEL          STANDARD;          PRT;      686 AA.
AC      Q10651; Q18583; Q95ZX1;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Beta-amyloid-like protein precursor.
GN      APL-1 OR C42D8.8.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE OF 6-686 FROM N.A.
RC      STRAIN=Bristol N2;
RX      MEDLINE=94089766; PubMed=8265668;
RA      Daigle I., Li C.;
RT      "apl-1, a Caenorhabditis elegans gene encoding a protein related to
RT      the human beta-amyloid protein precursor.";
RL      Proc. Natl. Acad. Sci. U.S.A. 90:12045-12049(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Bristol N2;
RA      Hallsworth K.;
RL      Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      REVISIONS, AND ALTERNATIVE SPLICING.
RA      Waterston R.;
RL      Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;

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CC      Name=a;
CC      IsoId=Q10651-1; Sequence=Displayed;
CC      Name=b;
CC      IsoId=Q10651-2; Sequence=VSP_000017;
CC      Note=No experimental confirmation available;
CC      -!- SIMILARITY: Belongs to the APP family.
CC      -----
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CC      -----
DR      EMBL; U00240; AAC46470.1; ALT_INIT.
DR      EMBL; U56966; AAA98722.1; -.
DR      EMBL; U56966; AAK68242.1; -.
DR      PIR; T15795; T15795.
DR      HSSP; P05067; 1MWP.
DR      WormPep; C42D8.8a; CE04209.
DR      WormPep; C42D8.8b; CE27845.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
KW      Signal; Transmembrane; Amyloid; Neurogenesis; Glycoprotein;
KW      Alternative splicing.
FT      SIGNAL      1      21      POTENTIAL.
FT      CHAIN      22      686      BETA-AMYLOID-LIKE PROTEIN.
FT      DOMAIN      22      621      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      622      642      POTENTIAL.
FT      DOMAIN      643      686      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN      205      228      ASP-RICH.
FT      DOMAIN      676      679      CLATHRIN-BINDING (POTENTIAL).
FT      CARBOHYD      84      84      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      201      201      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      249      249      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      417      417      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      VARSPLIC      538      539      Missing (in isoform b).
FT      /FTId=VSP_000017.
SQ      SEQUENCE      686 AA; 79434 MW; A0816858FDD48608 CRC64;

Query Match      22.4%; Score 817.5; DB 1; Length 686;
Best Local Similarity 29.1%; Pred. No. 3.9e-33;
Matches 222; Conservative 110; Mismatches 275; Indels 155; Gaps 22;

Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      :: || : : | | | | | | | | : | || | : | : | | : |
Db      6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA 63

Qy      61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      || | ||:|:: || : |||:| | : |:| :||: || | | || |: |
Db      64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

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